

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 12:51:18 ; Search time 41 Seconds
(without alignments)
816.669 Million cell updates/sec

Title: US-10-713-208-6
Perfect score: 1800
Sequence: 1 MAEIGEDLDKSDVSSLIFLM.....ITESKDMHFSSLGICILLDLVL 348
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	184.5	10.2	212	2 I67437	cysteine proteinas
2	184.5	10.2	277	2 S64710	cysteine proteinas
3	184.5	10.2	277	2 JC5410	CPP32 protein - mo
4	183.5	10.2	277	2 A55315	cysteine proteinas
5	180.5	10.0	452	2 JC6507	caspase-2 - rat
6	177.5	9.9	435	2 A54821	apoptosis regulato
7	169	9.4	312	2 B54821	ICE-LAP6 - human
8	161	8.9	416	2 G02635	interleukin-1-beta
9	149.5	8.3	182	2 I67436	interleukin-1-beta
10	138.5	7.7	418	2 B57511	interleukin-1-beta
11	136	7.6	383	2 A56084	interleukin-1-beta
12	134	7.4	454	2 JC7123	caspase-9 long cha
13	129.5	7.2	495	2 T20038	hypothetical prote
14	129.5	7.2	503	2 A49429	interleukin-1 beta
15	126.5	7.0	404	2 A42677	interleukin-1 beta
16	124.5	6.9	311	2 B56084	interleukin-1-beta
17	122	6.8	241	2 T30761	hypothetical prote
18	120	6.7	263	2 C56084	interleukin-1-beta
19	116	6.4	377	2 A57511	interleukin-1 beta
20	109.5	6.1	402	2 A46495	IL-1 beta converta
21	102	5.7	1537	2 F86509	conserved hypothet
22	102	5.7	1537	2 C81558	ct147 hypothethical
23	102	5.7	1537	2 H72112	assimilatory nitra
24	101.5	5.6	743	2 G83726	cag island protein
25	100	5.6	1819	2 A71928	oligodendropeptidase
26	98.5	5.5	613	2 A99552	hypothetical zinc
27	98.5	5.5	680	2 T41670	hypothetical zinc
28	98.5	5.5	1641	2 T10955	early nodulin bind
29	97.5	5.4	854	2 C83905	hypothetical prote

30 97.5 5.4 2104 2 T38774 myosin-3 heavy cha
31 97 5.4 892 2 AG1661 transcription regu
32 96.5 5.4 1287 2 T42658 hypothetical prote
33 96 5.3 488 2 T13385 hypothetical prote
34 95 5.3 892 2 A11289 transcription regu
35 95 5.3 1629 2 T06461 DNA-binding protei
36 94.5 5.2 344 2 B70136 flagellar motor sw
37 94 5.2 1713 2 A55347 adhesive ligand ep
38 94 5.2 2670 2 A46719 inositol 1,4,5-tri
39 94 5.2 2671 2 A49873 inositol 1,4,5-tri
40 94 5.2 4589 2 T14914 dynein beta heavy
41 93.5 5.2 1811 2 T39252 probable protein t
42 93 5.2 455 2 G70113 replicative DNA he
43 93 5.2 1265 2 T47626 structural mainten
44 93 5.2 1875 2 S38173 myosin-like protei
45 93 5.2 1927 2 G64585 cag pathogenicity

ALIGNMENTS

RESULT 1

I67437
cysteine proteinase (EC 3.4.22.-) P32 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I67437
R;Flaws, J.A.; Kugu, K.; Trbovich, A.M.; DeSanti, A.; Tilly, K.I.; Hirshfield, A.N.; Tilly, R.; Endocrinology 136, 5042-5053, 1995
A;Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cell nuloosa cells of the ovarian follicle.
A;Reference number: I53300; MUID:96042508; PMID:7588240
A;Accession: I67437
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-212 <RES>
A;Cross-references: UNIPROT:P55213; EMBL:U34685; NID:g1004370; PIDN:AAC52261.1; PID:g1004370
C;Keywords: cysteine proteinase; hydrolase

Query Match	10.2%	Score 184.5;	DB 2;	Length 212;
Best local similarity	29.1%;	Pred. No. 8.9e-07;		
Matches	60;	Conservative 36;	Mismatches 81;	Indels 29; Gaps 8;
QY	127	ERYKMKSLGICLIID-----CIGNETEL-----LRDTFTSLGYEVOKFLHLHLSM	172	
Db	5	DSYKMDYEMGLCIIINNNKFKSTGSGARNGCTDVDAANLRFTFMALKYEVNRKNKDLTR	64	
QY	173	HGISQLGQFACMPHERDYDSFVCLVSRGGSQSVYGVQTHSGSLPLHHRMFMGDS	232	
Db	65	EEIMELMDSVS-KEDHSKRSSFVCLVSHGDEGVIFG---TNGPVDLKKLTSPFRGDYCR	120	
QY	233	YLAGPKMFFIQYVYVSDGLEDSLSLLEVDGPKMKVFEKAKRGKGLCTVHREADFFWSLC	292	
Db	121	SLTGPKLFIQ---ACRGTELDSDG-IETSDGDDV--ACQKPV-----EADFLYAYS	169	
QY	293	TADMSLLEQSHSPSYLYQLCSQKLR	318	
Db	170	SAPGYVSWNSRGGSWFIOSLCAMLX	195	

RESULT 2

S64710
cysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster
C;Species: Crictetus griseus (Chinese hamster)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C;Accession: S64710; S72395
R;Wang, X.; Zelenski, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.
EMBO J. 15, 1012-1020, 1996
A;Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 during apoptosis.
A;Reference number: S64710; MUID:96183185; PMID:8605870
A;Accession: S64710
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA

A:Residues: 1-277 <WAW>
A:Cross-references: EMBL:U27463
R:Wang, X.
Submitted to the EMBL Data Library, May 1995
Reference number: S72395
A:Accession: S72395
A:Molecule type: mRNA
A:Residues: 1-79, 'A', '81-146, 'Y', '148-277 <WAW>
A:Cross-references: EMBL:U27463; NID:G1244443; PIDN:AAB01511.1; PID:G1244444
C:Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match 10.2%; Score 184.5; DB 2; Length 277;
Best Local Similarity 27.9%; Pred. No. 1.3e-06;
Matches 67; Conservative 36; Mismatches 94; Indels 43; Gaps 9;

QY 96 KSLKPSNNFREPEPVKKS-IQSEAFLPQSIPEERYKMKSKPLGLICLIID----- 144
Db 11 KSIK-----NFEVKTIHGSKMSDGIYLDSS-----YKMDYPMGVGCIINNNKFNHKTGM 61
QY 145 --CIGNETEL--LRDTFTSLGYEVQKFLHLSMHGISOILGQFACMPHEHRDYSFVCLVLS 200
Db 62 TPRSCTDVAALKREFMNLKYEVRNKNDLTREEIVELM-KNASKEDHSKRSSFVCLVLS 120
QY 201 RGSQSQVYGVQDTHSGPLHRRMPMGDSCPYLAKPKMFFIQ--NYVVSQGLEDSLS 258
Db 121 HGDGEGVIFGTD--GPIDLKLTYSFRGDRCSLIGKPKLFIQACRGTELDGCIETDSG 177
QY 259 LEVDGPAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSLLSQSHSSPSLYLQCLSKLR 318
Db 178 TEDDMTCQK-----IPVEADFLYAYSTAPGYYSWRNPKDGSWFIQSLCSMLK 224

RESULT 3
JC5410
CP32 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C:Accession: JC5410
R:Mukasa, T.; Urabe, K.; Momoi, M.Y.; Kimura, I.; Momoi, T.
Biochem. Biophys. Res. Commun. 231, 770-774, 1997
A:Title: Specific expression of CP32 in sensory neurons of mouse embryos and activation
A:Reference number: JC5410; MUID:97224429; PMID:9070890
A:Accession: JC5410
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-277 <MUK>
A:Cross-references: UNIPROT:P70677; DDBJ:D86352
A:Experimental source: embryo
C:Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons.

Query Match 10.2%; Score 184.5; DB 2; Length 277;
Best Local Similarity 28.9%; Pred. No. 1.3e-06;
Matches 67; Conservative 35; Mismatches 93; Indels 37; Gaps 11;

QY 103 NNFREPEV--KKSIOSEAFLPQSIPEERYKMKSKPLGLICLI-----DCIGN 148
Db 14 NNFVGTIHKSGSV-DSGIYLDSS-----YKMDYPMGICIIITNNKFNHKTGMSRSCT 67
QY 149 ETEL--LRDTFTSLGYEVQKFLHLSMHGISOILGQFACMPHEHRDYSFVCLVSRGSQS 206
Db 68 DVDANLRETFMGLKYEVRNKNDLTREEIMELMDSVS-KEDHSKRSSFVCLVLSHGDEGV 126
QY 207 VGVVDQTHSGPLHRRMPMGDSCPYLAKPKMFFIQNYVVSQGLEDSLSLEVDGPAM 266
Db 127 IFG---TNGPVDLKKLTSTFRGDYGRSLTGKPKLFIQ---ACRGTELDGCIETDSG- 178
QY 267 KNVEFKAQKRGCLCTVHREADFFWSLCTADMSLLSQSHSSPSLYLQCLSKLR 318
Db 179 -DEEMACQK-----IPVEADFLYAYSTAPGYYSWRNPKDGSWFIQSLCSMLK 224

cysteine proteinase (EC 3.4.22.-) CPP32 precursor - human
N:Alternate names: cysteine proteinase CPP32
C:Species: Homo sapiens (man)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C:Accession: A55315; S58899; I39005
R:Fernandes-Alnemri, T.; Litwack, G.; Alnemri, E.S.
J. Biol. Chem. 269, 30761-30764, 1994
A:Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elegans C-1
A:Reference number: A55315; MUID:95074098; PMID:7983002
A:Accession: A55315
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-277 <FER>
A:Cross-references: UNIPROT:P42574; GB:U13737; NID:G561665; PIDN:AAA65015.1; PID:G561666
R:Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant, M.; Yu, V.L.; Miller, D.K.
Nature 376, 37-43, 1995
A:Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammalian
A:Reference number: S58899; MUID:95319529; PMID:7596430
A:Accession: S58899
A:Molecule type: protein
A:Residues: 29-46;176-189, 'E', '191-193 <NIC>
R:Fewari, M.; Quan, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Poirier, Cell 81, 801-809, 1995
A:Title: Yama/CP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease t
A:Reference number: A56924; MUID:95292347; PMID:7774019
A:Accession: I39005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-189, 'E', '191-277 <RES>
A:Cross-references: EMBL:U26943; NID:G857568; PIDN:AAA74929.1; PID:G857569
C:Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query Match 10.2%; Score 183.5; DB 2; Length 277;
Best Local Similarity 26.4%; Pred. No. 1.5e-06;
Matches 64; Conservative 41; Mismatches 100; Indels 37; Gaps 7;

QY 98 LKDPNNFREPEPVK---KSIQSEAFLPQSIPEERYKMKSKPLGLICLIID----- 144
Db 1 MENTENSVDKSIKLEPKLIHGSESDSGISLDNSYKMDYPMGICIIINNNKFNHKTG 60
QY 145 ---CIGNETEL--LRDTFTSLGYEVQKFLHLSMHGISOILGQFACMPHEHRDYSFVCLV 199
Db 61 MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVS-KEDHSKRSSFVCLV 119
QY 200 SRGGSQVYGVQDTHSGPLHRRMPMGDSCPYLAKPKMFFIQ--NYVVSQGLEDS 257
Db 120 SHGEGIIIFG---TNGPVDLKKLTSTFRGDRCSLTGKPKLFIQACRGTELDGCIET 176
QY 258 LLEVDPAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSLLSQSHSSPSLYLQCLSK 317
Db 177 GVDDDMACHK-----IPVDADFLYAYSTAPGYYSWRNPKDGSWFIQSLCAML 223
QY 318 RQ 319
Db 224 KQ 225

RESULT 5
JC6507
caspase-2 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: JC6507
R:Sato, N.; Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.
Gene 202, 127-132, 1997
A:Title: Cloning and expression of the cDNA encoding rat caspase-2.
A:Reference number: JC6507; MUID:98087427; PMID:9427555
A:Accession: JC6507
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-452 <SAT>
A:Cross-references: UNIPROT:O55194; GB:U77933; NID:G2769705; PIDN:AAB96379.1; PID:G276970

RESULT 7
B54821
apoptosis regulator ICH-1, suppressive form S - human
C;Species: Homo sapiens (man)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
C;Accession: B54821
R;Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
Cell 78, 739-750, 1994
A;Title: Ich-1, an Ice/ced-3-related gene, encodes both positive and negative
A;Reference number: A54821; MUID:94373811; PMID:8087842
A;Accession: B54821
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-312 <WAN>
A;Cross-references: GB:U10322
C;Keywords: alternative splicing; apoptosis

Qy	42	L E K N I V A P D O L --- D L E K C L - K N I H R I D U K --- T K I Q Y K Q S V Q G A G T S Y R N V L Q A -	92
Dd	:	: : : :	:
Dd	:	: : : :	:
Dd	:	: : : :	:
Qy	9	L K O R V V A K O L L S E L L E H L E K D I I T L E M R E I Q A K V S F S Q N V L L N L L P K R G P Q A F	68
Qy	93	- A I O K S L K D P S N N P R E B P V K S I O E S E A F L P --- Q S I P ---	126
Dd	:	: : : :	:
Dd	:	: : : :	:
Qy	69	D A F C E A L R E T K O G H L E D W M L L T T S G L Q H V L P L S C D Y D L S U P P V C S E C P L Y K L R L S T D	128
Qy	127	--- E R Y K M K S P L G I C I I D C I - G N E T E L ---	152
Dd	:	: : : :	:
Dd	:	: : : :	:
Qy	129	T V E H S L N K D G P V C L Q V K P C T P B E Y O T H F O L A Y L R L Q S R P R G L A L V S N V H F T G E K E L E F R	188
Qy	153	-----L R D T F T S L G Y E V O K F L H L S M H G I S O I L G O F A C M P E H R D V D S F V C V L V S R G G	203
Dd	:	: : : :	:
Dd	:	: : : :	:
Qy	189	S G G V D H S T L V T L F K L G Y D V H V L C D Q T A Q E M Q E K L Q N F A Q L P A H R V T D S C I A L L S H G V	248
Qy	204	S Q S V Y G V D Q T H S G L P L H H I R M F M G D S C P Y L A G R P K M F F I Q	244
Dd	:	: : : :	:
Dd	:	: : : :	:
Dd	:	: : : :	:
Dd	249	E G A T Y G V D --G K L L O E V F O L F O N A N C P S I O N K P M F F I Q	287

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RESULT 8
G02635
ICE-LAP6 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C:Accession: G02635
R:Duan, H.; Orth, K.; Chinmoyan, A.M.; Poirier, G.G.; Froelich, C.J.; He, W.W.
submitted to the EMBL Data Library, April 1996
A:Reference number: H01513
A:Accession: G02635
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-416 <DUA>
A:Cross-references: EMBL:U56390; NID:g1336026; PIDN:AAC50640.1; PID:g1336027
Query Match 8.9%; Score 161; DB 2; Length 416;
Best Local Similarity 22.0%; Pred. No. 0.00013;
Matches 77; Conservative 60; Mismatches 149; Indels 64; Gaps 11
19 LMKDYMGRGKISKSEKSFLLDLVVELEKLNVLNPAQDQDLLEKLCIKNTHRIDLTKTKIQKYKOS 78

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Db 39 MIEDIQAGSGRRDQARQLIIDLETRGSA--LPLFISCLSDTQCDMLASFLRTNRQA 95
QY 79 VQAGAGSYRNVLQAAIQKSLKOP-----SNNREEPVKKSIQSEAFPLPS 124
Db 96 GKLSKPTLENLTPVVLIRPEIRKPEVLRPTPRVDIGSGGFGDVGALSLRG----- 148
QY 125 IPEERYKMKSPKLGICLIIDICIG--NETELLRDTFTSLGYEVQKFLHLSMHGSIQILGQF 182
Db 149 -ADLAILSWFCGCHCLLIINNVCRESGLRTFTGSNIDCEKLRFRFFSLHFWVEVKGL 207
QY 183 A-----CMPHRRDYDSFVCLVSRGSGSQS-----VYGVDTQTHSLP--LHHI 222
Db 208 TAKKMWLALLELARQDHGALDCCVVILSHGCOASHLQFPFAGVYGT-----GCPVSVEKI 263
QY 223 RRMFMGDCSPYLAGKPKMFQI-----NYVVSDDGLE-----SSLLEVDG--PAMKV 269
Db 264 VNIIFNGTSCPSGGKPKLFFIQACGGEQKDHGFVASTSPEDSPSGNPEPATPQEG 323
QY 270 EFKAQKRGGLCTVHREADFFWSLCTADMSLLEQSHSPSYLQCLSKLRQ 319
Db 324 RIFDQLDAISSLTPSPDIFVSYSTFPFVSWRDPKSGSWYVETLDDIFEQ 373
RESULT 9
I67436
interleukin-1-beta-converting enzyme and ced-3 homolog-1, long isoform - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I67436
R:Flaws, J.A.; Kugu, K.; Trbovich, A.M.; DeSanti, A.; Tilly, K.I.; Hirshfield, A.N.; Til
Endocrinology 136, 5042-5053, 1995
A:Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cel
nuloa cells of the ovarian follicle.
A:Reference number: I53300; MUID:96042508; PMID:7588240
A:Accession: I67436
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-182 <RES>
A:Cross-references: UNIPROT:P55215; EMBL:U34684; NID:g1004368; PIDN:AAC52260.1; PID:g100

Query Match 8.3%; Score 149.5; DB 2; Length 182;
Best Local Similarity 31.0%; Pred. No. 0.00033;
Matches 44; Conservative 18; Mismatches 61; Indels 19; Gaps 4;
QY 136 PLGICLIIDCI-----GNETE--LLRDTFTSLGYEVQKFLHLSMHGSIQILQ 181
Db 1 PGLALVMSNVHFTGKDLFRSGGDVHTTLVTLFKLGINVHVLYDQTAQEMQEKLN 60
QY 182 FACMPHRRDYDSFVCLVSRGSGSQSYGVVDQTHSGPLHHRMFMGDCSPYLAGKPKMF 241
Db 61 FAQLPAHRYTDSICVALLSHGVEGGYGV--GKLLQLQEVFLFDNANCPSLQNKPKMF 118
QY 242 FQNYVVSQGLQEDSSLLEVDG 263
Db 119 FIQ---ACRGDETRDGVDDQDG 137
RESULT 10
B57511
interleukin-1 beta converting enzyme (EC 3.4.22.-) ICErel-III - human
C:Species: Homo sapiens (man)
C:Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 09-Jul-2004
C:Accession: B57511; S62183
R:Munday, N.A.; Vaillancourt, J.P.; Ali, A.; Casano, F.J.; Miller, D.K.; Molineaux, S.M.
J. Biol. Chem. 270, 15870-15876, 1995
A:Title: Molecular cloning and pro-apoptotic activity of ICE-relIII, membe
A:Reference number: A57511; MUID:95318183; PMID:7797592
A:Accession: B57511
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-418 <MUN>
A:Cross-references: UNIPROT:P51878; GB:U28015; NID:g975300; PIDN:AAA5172.1; PID:g903938

R:Faucheu, C.; Blanchet, A.M.; Collard-Dutilleul, V.; Lalanne, J.L.; Diu-Hercend, A.
Eur. J. Biochem. 236, 207-213, 1996
A:Title: Identification of a cysteine protease closely related to interleukin-1-beta-con
A:Reference number: S62183; MUID:96184899; PMID:8617266
A:Accession: S62183
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 55-317, 'L', 319-418 <FAU>
A:Cross-references: EMBL:X94993; NID:g1155085; PIDN:CAA64450.1; PID:g1155086
C:Keywords: cysteine proteinase; hydrolase
Query Match 7.7%; Score 138.5; DB 2; Length 418;
Best Local Similarity 23.4%; Pred. No. 0.0069;
Matches 77; Conservative 52; Mismatches 125; Indels 75; Gaps 16;
QY 10 KSDVSSLIPLMKD-----YMGRG-----KISKEKSFLDLVLEKLNVLAPDQDLLE 57
Db 50 KKTVMKLEVLGKDVHGVFNVLAKHDVLTLEKEEKKKYDAKIEDKALILV-----DSL 104
QY 58 KCLKNHRIIDLTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNNF-----REBPVKK 112
Db 105 K-NRVAHQMFQT--LLNWDQKI-----TSVKPLQIEAGPPESAESTNLIKCPREFLRL 158
QY 113 SIQSEAFPLPOSIPEERYKMKSPKLGICLI-----DCIGNETELLRDT 156
Db 159 CKKNHDEIVPIKKREDRRR-----LALIICNTKFDHLPARGAHYDIVG-----MKEL 206
QY 157 FTSLSGVEQKFLHLSMHGSIQILGOFACMPHERDYDSFVCLVSRGSGSQSYGV--DQT 213
Db 207 LQGLGYTVDEKNLTARDMESVLRFAARPEKHSSDSTFLVLMSHGILEGICGTAHKKKK 266
QY 214 HSGPLHHRMFMGDCSPYLAGKPKMFQIYNYVVSQDQ-----LEDS--SLLEVDGPA 265
Db 267 PDVLLYDIFIQIFNNRNCLSLKDKEKVIIVQ---ACRGEKHGELVWRDSPASLAVISSQS 323
QY 266 MNVEFKAKQKGLCTVHREADFFWSLCTA 294
Db 324 SENLEADS-----VCKIHBEKDPI-AFCSS 347
RESULT 11
A56084
interleukin-lbta converting enzyme beta isozyme - human
C:Species: Homo sapiens (man)
C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C:Accession: A56084
R:Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
J. Biol. Chem. 270, 4312-4317, 1995
A:Title: Cloning and expression of four novel isoforms of human interleukin-lbta convert
A:Reference number: A56084; MUID:95181414; PMID:7876192
A:Accession: A56084
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-383 <ALN>
A:Cross-references: UNIPROT:P29466; GB:U13697; NID:g717039; PIDN:AAC50107.1; PID:g717040
C:Genetics:
A:Gene: IL1BCE
C:Keywords: alternative splicing
Query Match 7.6%; Score 136; DB 2; Length 383;
Best Local Similarity 24.0%; Pred. No. 0.0095;
Matches 81; Conservative 54; Mismatches 145; Indels 58; Gaps 12;
QY 24 MCRGKISKEKSFLDLVLEKLNVLAPDQDLLEKCLKNHRIIDLTKIQKYKQSVQ--- 80
Db 17 MEGGTIN---GLLDELQTRVLUNKEMEKKRENATVMDKTALIDSVIPKGAQACQICI 73
QY 81 -----GAGTSYRNVLQAAIQKSLKDPNNFPEEPVKK-SIQSEAFPLQSIPEERY 130
Db 74 TYICEEDSVLACTGLGSAAPQAVQDNPAIMPPTSSGSEGNVKLCSLEAQRWKQGAETYP 133
QY 131 KM-KSKPKLGICLI-----DCI-----GNETELLRDT--FTSLGYEVQKFLHLSMHGSIQI 178

Db 134 IMDKSRTRLALICNEEPDSIPRR7GAEDVITGMTMLLQNLGYSYDVKKNL7ASDWTTE 193
QY 179 LQOFACWPEHRDVSFVCLVSRGGSQSVYG---VDQTHSGLPPLHHIRRMFMGDSQPYLA 235
Db 194 LEAFARPEHKTSDSTFLVFMHSGIREGICKKHSEQVPDILQLNAIFNMLNTKNCPSLK 253
QY 236 GKPKMFFIO-----NYVSDGQLEDSSLLLEVDGPAKMKVFEKAKRGKGLCTVH 282
Db 254 DRPKVILIIQACRGSQGVVWFKDSVGSVGNLSLPTTEEFEDDAIK-----AH 301
QY 283 READFFWLSCTADMSLLEQSH--SSPSLYLQCLSKQLRQ 319
Db 302 IEKDFI-AFCSSPPDNVSMRHPTMGVFIGRLIEHQE 338
RESULT 12
JC7123
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: JC7123
R:Fujita, E.; Jinbo, A.; Maturaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T.
Biochem. Biophys. Res. Commun. 264, 550-555; 1999
A:Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9.
A:Reference number: JC7123; MUID:20001956; PMID:10529400
A:Accession: JC7123
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-454 <FUF>
A:Cross-references: UNIPROT:Q9R0T0; DDBJ:AB019600; NID:G6440941; PID:G6440942
Query Match 7.4%; Score 134; DB 2; Length 454;
Best Local Similarity 33.1%; Pred. No. 0.017;
Matches 45; Conservative 15; Mismatches 52; Indels 24; Gaps 6;
QY 130 YKMKSKPLGICLIID----C----IGNET-----ELLRDTFTSLGVEYQKFLHLSMHGI 175
Db 191 YLDSOPCGHCLLIINNWNFCRSGGLGTRTGSNIDRKLEHRFWLRFVVEVKNLDTAKKM 250
QY 176 SQILGQFACWPEHRDVSFVCLVSRGGSQ-----YGVQDQTHSGLPPLHHIRRMFMG 228
Db 251 VTALMEMA-HRNHRALDCFVVVILSHGQASHQFPFCAVVGTD--GCSVSIKIVNIENG 307
QY 229 DSCPYLAGKPKMFFIQ 244
Db 308 SGCPSLGGKPKLFFIQ 323
RESULT 13
T20038
hypotheetical protein C48D1.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T20038
R:Burton, J.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19214
A:Accession: T20038
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-495 <WIL>
A:Cross-references: EMBL:Z61049; PIDN:CA802848.1; GSPDB:GN00022; CBSP:C48D1.2
A:Experimental source: clone C48D1
C:Genetics:
A:Gene: CBSP:C48D1.2
A:Map position: 4
A:Introns: 44/3; 93/2; 178/1; 288/3; 360/1; 402/3; 466/1
Query Match 7.2%; Score 129.5; DB 2; Length 495;
Best Local Similarity 24.0%; Pred. No. 0.042;
Matches 63; Conservative 37; Mismatches 86; Indels 77; Gaps 12;
QY 70 TKIQKYQSVQAGTGYRNVLQAAIQKS-----LKDPSNNFREEP----- 109

Db 126 TRVHRDSVSSVSTSYQDIYSRARSRSRALHSSDRHNSPPVNAFPSPSSANSF 185
QY 110 -----VKKSIQSEAFLPQSIPEE-----RYKMKSKPLGIC 140
Db 186 TCSSLSGSSSRNRSFASKGPTQYIFHEEDMNFVDAPTISRVDKTYRNFSSPRGMC 245
QY 141 LIID-----CIGNETELLRDTFTSL-----GYEVOKFLHLSMHGISQILGQFACWPEHR 189
Db 246 LIINNEHFQMPTRNGTKADKDNLTNLFRCMGVTVICKONLTGRGMLLTIRDA---KHE 302
QY 190 DY-DSFVCLVSRGGSQSVYGVQDTHSGLP--HHIRRMFMGDSQPYLAGKPKMFFIQNY 246
Db 303 SHGDSAILVILSHGENVIIGVDD-----IPISTHEIYDLNANAPRLANKPKIVFVQ-- 356
QY 247 VVSDGQLEDSS---LLEVDG-PA 265
Db 357 -ACRGERDRNGFPVLDSVDGVPA 378
RESULT 15
A42677
interleukin-1 beta converting enzyme (EC 3.4.22.-) - human

Db 125 TRVHRDSVSSVSTSYQDIYSRARSRSRALHSSDRHNSPPVNAFPSPSSANSF 184
QY 110 -----VKKSIQSEAFLPQSIPEE-----RYKMKSKPLGIC 140
Db 185 TCSSLSGSSSRNRSFASKGPTQYIFHEEDMNFVDAPTISRVDKTYRNFSSPRGMC 244
QY 141 LIID-----CIGNETELLRDTFTSL-----GYEVOKFLHLSMHGISQILGQFACWPEHR 189
Db 245 LIINNEHFQMPTRNGTKADKDNLTNLFRCMGVTVICKONLTGRGMLLTIRDA---KHE 301
QY 190 DY-DSFVCLVSRGGSQSVYGVQDTHSGLP--HHIRRMFMGDSQPYLAGKPKMFFIQNY 246
Db 302 SHGDSAILVILSHGENVIIGVDD-----IPISTHEIYDLNANAPRLANKPKIVFVQ-- 355
QY 247 VVSDGQLEDSS---LLEVDG-PA 265
Db 356 -ACRGERDRNGFPVLDSVDGVPA 377
RESULT 14
A49429
interleukin-1 beta-converting enzyme homolog CED-3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A49429; T37312
R:Yuan, J.; Shaham, S.; Ledoux, S.; Ellis, H.M.; Horvitz, H.R.
Cell 75, 641-652, 1993
A:Title: The C. elegans cell death gene ced-3 encodes a protein similar to mammalian inter-
A:Reference number: A49429; MUID:94061982; PMID:8242740
A:Accession: A49429
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-503 <YUA>
A:Cross-references: UNIPROT:P42573; GB:L29052; NID:G6503232; PIDN:AAA27982.2; PID:G6503232
A:Note: sequence extracted from NCBI backbone (NCBIN:139825, NCBIIP:139826)
A:Accession: T37312
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-417,'R',419-503 <YU2>
A:Cross-references: EMBL:L29052; PIDN:AAA27982.1
C:Genetics:
A:Gene: ced-3
A:Introns: 45/3; 94/2; 179/1; 289/3; 361/1; 403/3; 483/3
Query Match 7.2%; Score 129.5; DB 2; Length 503;
Best Local Similarity 24.0%; Pred. No. 0.043;
Matches 63; Conservative 37; Mismatches 86; Indels 77; Gaps 12;
QY 70 TKIQKYQSVQAGTGYRNVLQAAIQKS-----LKDPSNNFREEP----- 109
Db 126 TRVHRDSVSSVSTSYQDIYSRARSRSRALHSSDRHNSPPVNAFPSPSSANSF 185
QY 110 -----VKKSIQSEAFLPQSIPEE-----RYKMKSKPLGIC 140
Db 186 TCSSLSGSSSRNRSFASKGPTQYIFHEEDMNFVDAPTISRVDKTYRNFSSPRGMC 245
QY 141 LIID-----CIGNETELLRDTFTSL-----GYEVOKFLHLSMHGISQILGQFACWPEHR 189
Db 246 LIINNEHFQMPTRNGTKADKDNLTNLFRCMGVTVICKONLTGRGMLLTIRDA---KHE 302
QY 190 DY-DSFVCLVSRGGSQSVYGVQDTHSGLP--HHIRRMFMGDSQPYLAGKPKMFFIQNY 246
Db 303 SHGDSAILVILSHGENVIIGVDD-----IPISTHEIYDLNANAPRLANKPKIVFVQ-- 356
QY 247 VVSDGQLEDSS---LLEVDG-PA 265
Db 357 -ACRGERDRNGFPVLDSVDGVPA 378
RESULT 15
A42677
interleukin-1 beta converting enzyme (EC 3.4.22.-) - human

C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: A54263; A42677; S21734; S24164
R: Cerretti, D.P.; Hollingsworth, L.T.; Kozlosky, C.J.; Valentine, M.B.; Shapiro, D.N.; M
Genomics 20, 468-473, 1994
A:Title: Molecular characterization of the gene for human interleukin-beta converting e
A:Reference number: A54263; MUID:94307734; PMID:8034320
A:Accession: A54263
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-404 <CE2>
A:Cross-references: UNIPROT:P29466; GB:I27475
R: Cerretti, D.P.; Kozlosky, C.J.; Mosley, B.; Nelson, N.; Van Ness, K.; Greenstreet, T.A
Science 256, 97-100, 1992
A:Title: Molecular cloning of the interleukin-beta converting enzyme.
A:Reference number: A42677; MUID:92229430; PMID:1373520
A:Accession: A42677
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-404 <CER>
A:Cross-references: GB:M87507; NID:9435598; PIDN:AAA66942.1; PID:gl86286
R: Thornberry, N.A.; Bull, H.G.; Calaycay, J.R.; Chapman, K.T.; Howard, A.D.; Koestura, M.
J.; Ding, G.J.F.; Egger, L.A.; Gaffney, E.P.; Limjuco, G.; Palyha, O.C.; Raju, S.M.; Rol
cci, M.J.
Nature 356, 768-774, 1992
A:Title: A novel heterodimeric cysteine protease is required for interleukin-beta proce
A:Reference number: S21734; MUID:92244338; PMID:1574116
A:Accession: S21734
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-404 <THO>
A:Cross-references: EMBL:X65019; NID:g33792; PIDN:CAA46153.1; PID:g33793
R: Kronheim, S.R.; Muma, A.; Greenstreet, T.; Glackin, P.J.; van Ness, K.; March, C.J.;
Arch. Biochem. Biophys. 296, 698-703, 1992
A:Title: Purification of interleukin-beta converting enzyme, the protease that cleaves
A:Reference number: S24164; MUID:92337439; PMID:1321594
A:Accession: S24164
A:Status: preliminary
A:Molecule type: protein
A:Residues: 120-135, 'AX', 138-139, 'X', 141-142 <KRO>
C:Genetics:
A:Gene: GDB:IL1BC
A:Cross-references: GDB:132368; OMIM:147678
A:Map position: 11q23-11q23
C:Keywords: cysteine proteinase; hydrolase

Query Match 7.0%; Score 126.5; DB 2; Length 404;
Best Local Similarity 23.1%; Pred. No. 0.054;
Matches 83; Conservative 56; Mismatches 141; Indels 79; Gaps 14;

QY 24 MGRGKTSKEKSFLLVVELEKLNVLAPDQDLLEKCLKNHRIIDLTKIKYKQSVQ--- 80
DB 17 MGEETIN---GLLDELLQTVLNVKEEMKVKRENATVMDKTRALIDSVIPKGAQACQICI 73
QY 81 -----GAGT-----SYRNVLOA-----AIQSKLKDPSNNFREEPV 110
DB 74 TYICEEDSVYLAGTGLGLSADQTSGLNLMQDSQGLSVFPAPQAVQDNPAIMPSTSSGSEGNV 133
QY 111 KK-SIOESEAFLPOSIPERYKM-KSKPLGICLI-----DCI-----GNETELLRT--F 157
DB 134 KLCSEARQRIWKQKGAETIYPMDKSRTSLALIIINEEFDSPRRGTGAEDVITGMTMLL 193
QY 158 TSLGYEVQKFLHLSMHGISQILQGFACMPEDRDYDSFVCLVSVRGGSSQSVYG---VDQTH 214
DB 194 QNLGYSVDVKKNLTASDMTELEAFAPRPHKTSSTFLVFMHSHGREGICGKXSEQVP 253
QY 215 SGLPLHHIRRMFGDSCPYLAGKPKMFFIQ-----NYVVSQGLDSSLLLEV 261
DB 254 DILQLNAIFNMLNTKNCPSLKDKPKVIIQACRGSDPGVWVFKDSVGVSGNLSLPTTEEF 313
QY 262 DGPAMKRVFKAKRGKLCIVHREADFWSLCTADMSLLEQSH--SSPSLYLQCLSQKLQ 319
DB 314 EDDAIKK-----AHIEKDFI-AFCSSTPDNVSWRHFTMGSVFGRLEHMQE 359

Search completed: June 20, 2005, 13:06:07
Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 12:50:04 ; Search time 174 Seconds
(without alignments)
1024.158 Million cell updates/sec

Title: US-10-713-208-6
Perfect score: 1800
Sequence: 1 MAEIGEDLDKSDVSSLIPLM.....ITKMDHFFSLGCLLDVL 348

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1635	90.8	480	1	CFLA HUMAN	O15519 h casp8 and
2	1208	67.1	487	2	O6QN97	O6qn97 sus scrofa
3	1018	56.6	481	2	O812G4	O81294 mus musculus
4	1006.5	55.9	484	1	CFLA MOUSE	O35732 m casp8 and
5	600	33.3	497	2	O6NTR7	O6ntr7 xenopus lae
6	471	26.2	418	2	O8UVG5	O8uvg5 brachydanio
7	403.5	22.4	219	2	O6QN98	O6qn98 sus scrofa
8	345	19.2	218	2	O99WZ5	O99wz5 rattus norv
9	318.5	17.7	482	2	O9JHX4	O9jhx4 rattus norv
10	313	17.4	479	1	ICB8 HUMAN	O14790 h caspase-8
11	302.5	16.8	482	2	O90WU1	O90wu1 gallus gall
12	297	16.5	480	1	ICB8 MOUSE	O89110 mus musculus
13	277	15.4	78	2	O8MJ18	O8mj18 macaca mula
14	270	15.0	512	2	O6PAD9	O6pad9 xenopus lae
15	267	14.8	520	2	O9IB62	O9ib62 xenopus lae
16	265.5	14.8	476	2	O66119	O66119 brachydanio
17	265.5	14.8	476	2	O9IB73	O9ib73 brachydanio
18	248.5	13.8	521	1	ICB8 HUMAN	O92851 homo sapien
19	248.5	13.8	522	2	O8IU05	O8iup5 homo sapien
20	244	13.6	478	2	O6KFE2	O6kfe2 homo sapien
21	235	13.1	455	2	O6KFE3	O6kfe3 homo sapien
22	233	12.9	500	2	O9IB64	O9ib64 xenopus lae
23	214	11.9	283	2	O93417	O93417 gallus gall
24	213	11.8	366	2	O6E5N8	O6e5n8 ictalurus p
25	210.5	11.7	496	2	O81749	O81749 suberites d
26	199	11.1	293	1	ICB8 HUMAN	P55212 homo sapien
27	199	11.1	303	2	O9IB66	O9ib66 xenopus lae
28	198.5	11.0	400	2	O8ITP2	O8itp2 brachydanio
29	195.5	10.9	424	1	ICB2 CHICK	O98943 gallus gall
30	193.5	10.8	277	1	ICB3_PIG	O95nd5 sus scrofa
31	192.5	10.7	318	2	O9IB65	O9ib65 xenopus lae

32	192	10.7	277	1	ICB3 CANFA	O8mti5 canis famil
33	190.5	10.6	317	2	O6DCI2	O6dc12 xenopus lae
34	190	10.6	328	2	O8ITP3	O8itp3 brachydanio
35	189.5	10.5	277	1	ICB3_FELCA	O8mjul felis silve
36	188.5	10.5	277	1	ICB3_MOUSE	P70677 mus musculus
37	187.5	10.4	302	2	O918S9	O9189 oncorhynch
38	186.5	10.4	280	2	O8JIS9	O8jia9 oryzias lat
39	185.5	10.3	277	1	ICB3_RAT	P55213 rattus norv
40	185.5	10.3	282	1	ICB3_XENLA	P55866 xenopus lae
41	184.5	10.2	182	2	O77623	O77623 ovis aries
42	184	10.2	290	2	O8JIS8	O8jia8 oryzias lat
43	183.5	10.2	277	1	ICB3_CRILO	O60431 cricetus lat
44	183.5	10.2	277	1	ICB3_HUMAN	P42574 homo sapien
45	182.5	10.1	277	2	O6JH80	O6jhr80 cricetus lat

ALIGNMENTS

RESULT 1

ID	CFLA_HUMAN	STANDARD	PRT	480 AA
AC	O15519; O14673; O14674; O15137; O15138; O15356; O15510; O43618; O43619; O43620; O60458; O60459; O96TB4; Q9UEW1;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	CASP8 and FADD-like apoptosis regulator precursor (Cellular FLICE-like inhibitory protein) (c-FLIP) (Caspase-eight-related protein) (Casper)			
DE	(Caspase-like apoptosis regulatory protein) (CLARP) (MACH-related inducer of toxicity) (MRIT) (Caspase homolog) (CASH) (inhibitor of FLICE) (i-FLICE) (FADD-like antiapoptotic molecule 1) (Flame-1) (Usurpin)			
GN	Name=CFLAR; Synonyms=CASH, CLARP, MRIT;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC				
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 13 AND 14), AND MUTAGENESIS OF TYR-360.			
RC	TISSUE=Embryonic kidney, and Umbilical vein endothelial cells;			
RX	MEDLINE=97352452; PubMed=9208847; DOI=10.1016/S1074-7613(00)80450-1;			
RA	Shu H.-B., Halpin D.R., Goeddel D.V.;			
RT	"Casper is a FADD- and caspase-related inducer of apoptosis.";			
RL	Immunity 6:751-763(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).			
RX	MEDLINE=97470967; PubMed=9326610; DOI=10.1073/pnas.94.21.11333;			
RA	Han D.K.M., Chaudhary P.M., Wright M.E., Friedman C., Frask B.J., Riedel R.T., Baskin D.G., Schwartz S.M., Hood L.;			
RA	"MRIT, a novel death-effector domain-containing protein, interacts with caspases and BclXL and initiates cell death.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 94:11333-11338(1997).			
RL	[3]			
RN	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RP	TISSUE=Periphera blood lymphocytes;			
RC	MEDLINE=97360133; PubMed=9217161; DOI=10.1038/40657;			
RX	Immler M., Thome M., Hahne M., Schneider P., Hofmann K., Steiner V., Bodmer J.-L., Schroeter M., Burns K., Mattmann C., Rimoldi D., French J.E., Tschopp J.;			
RA	"Inhibition of death receptor signals by cellular FLIP.";			
RT	Nature 388:190-195(1997).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 8; 9 AND 10), AND MUTAGENESIS OF ASP-376.			
RC	TISSUE=T-cell;			
RX	MEDLINE=97373543; PubMed=9228018; DOI=10.1074/jbc.272.30.19542;			
RA	Srinivasula S.M., Ahmad M., Oltfille S., Bullrich F., Banks S., Wang Y., Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J., Armstrong R.C., Alnemri E.S.;			
RA	"FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates Fas/TNFR1-induced apoptosis.";			
RT				

RL J. Biol. Chem. 272:18542-18545(1997).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Umbilical vein endothelial cells;
 RX MEDLINE=97362203; PubMed=9211860; DOI=10.1074/jbc.272.28.17255;
 RA Hu S., Vincenz C., Ni J., Gentz R., Dixit V.M.;
 RT "I-FLICE, a novel inhibitor of tumor necrosis factor receptor-1- and
 CD-95-induced apoptosis.";
 RL J. Biol. Chem. 272:17255-17257(1997).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORMS 4; 5; 6 AND 7).
 RA Hu S., Dixit V.M.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 11 AND 12).
 RC TISSUE=Kidney;
 RX MEDLINE=99218584; PubMed=10200473;
 RA Rasper D.M., Vaillancourt J.P., Hadano S., Houtzager V.M., Seiden I.,
 Keen S.L.C., Tawa P., Xanthoudakis S., Nasir J., Martindale D.,
 Koop B.F., Peterson E.P., Thornberry N.A., Huang J., MacPherson D.P.,
 Black S.C., Hornung F., Lenardo M.J., Hayden M.R., Roy S.,
 Nicholson D.W.;
 RA "Cell death attenuation by 'Usurpin', a mammalian DED-caspase
 homologue that precludes caspase-8 recruitment and activation by the
 CD-95 (Fas, APO-1) receptor complex.";
 RL Cell Death Differ. 5:271-288(1998).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Skin fibroblast;
 RX MEDLINE=97426025; PubMed=9289491; DOI=10.1074/jbc.272.32.19641;
 RA Goltsvev Y.V., Kovalenko A.V., Arnold E., Varfolomeev E.E.,
 Brodianskii V.M., Wallach D.;
 RA "CASH, a novel caspase homologue with death effector domains.";
 RL J. Biol. Chem. 272:19641-19644(1997).
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Colon carcinoma;
 RX MEDLINE=98021435; PubMed=9380701; DOI=10.1073/pnas.94.20.10717;
 RA Inohara N., Koseki T., Hu Y., Chen S., Nunez G.;
 RT "CLARP, a death effector domain-containing protein interacts with
 caspase-8 and regulates apoptosis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
 RN [10]
 RP SEQUENCE FROM N.A. (ISOFORM 11).
 RX MEDLINE=21100893; PubMed=11161814; DOI=10.1006/geno.2000.6392;
 RA Hadano S., Yanagisawa Y., Staag J., Fichter K., Nasir J.,
 Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
 Ikeda J.-E., Hayden M.R.;
 RA "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,
 and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
 critical region at chromosome 2q33-q34: candidate genes for ALS2.";
 RL Genomics 71:200-213(2001).
 RN [11]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Lymph;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Deje J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Datsenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Viallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [12]
 RP MEDLINE=99098997; PubMed=9889531;
 RX Scaffidi C., Schmitz I., Krammer P.H., Peter M.E.;
 RA "The role of c-FLIP in modulation of CD95-induced apoptosis.";
 RL J. Biol. Chem. 274:1541-1548(1999).
 RN [13]
 RP INDUCTION.
 RX MEDLINE=99244884; PubMed=10227994;
 RA Algeciras-Schmich A., Griffith T.S., Lynch D.H., Paya C.V.;
 RT "Cell cycle-dependent regulation of FLIP levels and susceptibility to
 Fas-mediated apoptosis.";
 RL J. Immunol. 162:5205-5211(1999).
 RN [14]
 RP SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
 RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
 RA Hillman R.T., Green R.E., Brenner S.E.;
 RA "An unappreciated role for RNA surveillance.";
 RL Genome Biol. 5:RESEARCH008.16(2004).
 CC -!- FUNCTION: Apoptosis regulator protein which may function as a
 crucial link between cell survival and cell death pathways in
 mammalian cells. Acts as an inhibitor of TNFRSF6 mediated
 apoptosis. A proteolytic fragment (p43) is likely retained in the
 death-inducing signaling complex (DISC) thereby blocking further
 recruitment and processing of caspase-8 at the complex. Full
 length and shorter isoforms have been shown either to induce
 apoptosis or to reduce TNFRSF6-triggered apoptosis. Lacks enzymatic
 (caspase) activity.
 CC -!- SUBUNIT: TNFRSF6 stimulation triggers recruitment to the death-
 inducing signaling complex (DISC) formed by TNFRSF6, FADD and
 caspase-8. A proteolytic fragment (p43) stays associated with the
 DISC. Also interacts with caspase-10, caspase-3, TRAF1, TRAF2 and
 Bcl-X(L) (in vitro).
 CC -!- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=14;
 Name=1; Synonyms=FLIP-L, CLARP1, MRIT alpha-1, CASH alpha, I-FLICE
 1, FLAME-1 gamma, Usurpin alpha;
 Name=2; Synonyms=FLIP-S, CLARE2, MRIT beta-1, CASH beta;
 IsoId=O15519-2; Sequence=VSP_000828, VSP_000829;
 Name=3; Synonyms=MRIT alpha-2;
 IsoId=O15519-3; Sequence=VSP_000824, VSP_000838;
 Name=4; Synonyms=I-FLICE 2;
 IsoId=O15519-4; Sequence=VSP_000825;
 Name=5; Synonyms=I-FLICE 3;
 IsoId=O15519-5; Sequence=VSP_000840;
 Name=6; Synonyms=I-FLICE 4;
 IsoId=O15519-6; Sequence=VSP_000826, VSP_000841;
 Name=7; Synonyms=I-FLICE 5;
 IsoId=O15519-7; Sequence=VSP_000824, VSP_000827, VSP_000838;
 Name=8; Synonyms=Flame-1 alpha;
 IsoId=O15519-8; Sequence=VSP_000830;
 Name=9; Synonyms=Flame-1 beta;
 IsoId=O15519-9; Sequence=VSP_000830, VSP_000836, VSP_000837;
 Note=May be produced at very low levels due to a premature stop
 codon in the mRNA, leading to nonsense-mediated mRNA decay;
 Name=10; Synonyms=Flame-1 delta;
 IsoId=O15519-10; Sequence=VSP_000834, VSP_000835;
 Name=11; Synonyms=Usurpin beta;
 IsoId=O15519-11; Sequence=VSP_000838;
 Name=12; Synonyms=Usurpin gamma;
 IsoId=O15519-12; Sequence=VSP_000832, VSP_000833;
 Name=13;
 IsoId=O15519-13; Sequence=VSP_000831;
 Name=14;
 IsoId=O15519-14; Sequence=VSP_000839;
 CC -!- TISSUE SPECIFICITY: Widely expressed. Higher expression in
 skeletal muscle, pancreas, heart, kidney, placenta, and peripheral
 blood leukocytes. Also detected in diverse cell lines. Isoform 8
 is predominantly expressed in testis and skeletal muscle.

CC -!- INDUCTION: Repressed by IL-2 after TCR stimulation, during
 CC progression to the S-phase of the cell cycle.

Query Match 90.8%; Score 1635; DB 1; Length 480;
 Best Local Similarity 94.1%; Pred. No. 4.3e-109;
 Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSILFLMKDYMGRGKISKESFLLDVVELEKLNIVAPDQDLLEKCL 60
 DB MAEIGEDLDKSDVSSILFLMKDYMGRGKISKESFLLDVVELEKLNIVAPDQDLLEKCL 156

QY 61 KNHRIIDLTKIKYKQSVQAGTSTYRNVLQAAIQKSLKDPNSNFR----- 106
 DB KNHRIIDLTKIKYKQSVQAGTSTYRNVLQAAIQKSLKDPNSNFR----- 216

QY 107 -----EPVVKSIQESFAFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTFTSLGY 162
 DB LGAAQSPVVKSIQESFAFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTFTSLGY 276

QY 163 EVQKFLHLSMHGISTQILGQFACMPHEDYDSFVCLVSRGSGSVYGVDTHTSGLPPLHHI 222
 DB EVQKFLHLSMHGISTQILGQFACMPHEDYDSFVCLVSRGSGSVYGVDTHTSGLPPLHHI 336

QY 223 RRMFMGSDCPYLAKGPKMFQIYQNVVSDGOLEDSSLLVEDGPKMKVFEKAKRGKGLCTVH 282
 DB RRMFMGSDCPYLAKGPKMFQIYQNVVSDGOLEDSSLLVEDGPKMKVFEKAKRGKGLCTVH 396

QY 283 READFFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 321
 DB READFFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 435

RESULT 2

Q6QN97

ID Q6QN97 PRELIMINARY; PRT; 487 AA.

AC Q6QN97

DT 05-JUL-2004 (T-EMBLrel. 27, Created)

DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)

DE Cellular FLUICE-like inhibitory protein long form.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RA Goto Y., Maeda A., Matsuda F., Inoue N., Manabe N.;

RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

DR ENBL; AY533021; AAS22337.1; -

DR HSSP; P55211; IuXQ.

DR GO; GO:0030693; F:caspace activity; IEA.

DR GO; GO:0005515; F:protein binding; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR GO; GO:0042381; P:regulation of apoptosis; IEA.

DR InterPro; IPR011029; DEATH_like.

DR InterPro; IPR001875; DED.

DR InterPro; IPR001309; ICE_p20.

DR InterPro; IPR002398; Peptidase_C14.

DR Pfam; PF01335; DED; 2.

DR SMART; SM00115; CASC; 1.

DR PROSITE; PS50208; CASPASE_P20; 1.

DR PROSITE; PS50168; DED; 2.

SQ SEQUENCE 487 AA; 56000 MW; 067BE3618E9C0E7 CRC64;

Query Match 67.1%; Score 1208; DB 2; Length 487;

Best Local Similarity 69.5%; Pred. No. 2e-78;

Matches 237; Conservative 42; Mismatches 42; Indels 20; Gaps 2;

QY 1 MAEIGEDLDKSDVSSILFLMKDYMGRGKISKESFLLDVVELEKLNIVAPDQDLLEKCL 60
 DB MAEIGEDLDKSDVSSILFLMKDYMGRGKISKESFLLDVVELEKLNIVAPDQDLLEKCL 161

QY 61 KNHRIIDLTKIKYKQSVQAGTSTYRNVLQAAIQKSLKDPNSN----- 104
 DB KNHRIIDLTKIKYKQSVQAGTSTYRNVLQAAIQKSLKDPNSN----- 221
 QY 105 -----FREEPVKSIQESFAFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTFTSL 160
 DB GHPDFORDPVKTSIQESGAFLQLHQVPEERYKMKSKPLGICLIIDICIGNETELLRTFTSL 281
 QY 161 GYEVQKFLHLSMHGISTQILGQFACMPHEDYDSFVCLVSRGSGSVYGVDTHTSGLPPLH 220
 DB GYEVQKFLHLSMHGISTQILGQFACMPHEDYDSFVCLVSRGSGSVYGVDTHTSGLPPLD 341
 QY 221 HRRFMGSDCPYLAKGPKMFQIYQNVVSDGOLEDSSLLVEDGPKMKVFEKAKRGKGLCT 280
 DB HRRFMGSDCPYLAKGPKMFQIYQNVVSDGOLEDSSLLVEDGPKMKVFEKAKRGKGLCT 401
 QY 281 VHEADFFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 321
 DB VHEADFFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 442

RESULT 3

Q812G4

ID Q812G4 PRELIMINARY; PRT; 481 AA.

AC Q812G4

DT 01-JUN-2003 (T-EMBLrel. 24, Created)

DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)

DE CASP and FADD-like apoptosis regulator, isoform 1.

GN Name=Cflar;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Mammary tumor;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Mammary tumor;

RA Strausberg R.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR ENBL; BC029223; AAB29223.1; -

DR HSSP; Q9COK4; 1QTN.

DR MGD; MGI:1336166; Cflar.

DR GO; GO:0030693; F:caspace activity; IEA.

DR GO; GO:0005515; F:protein binding; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR GO; GO:0042381; P:regulation of apoptosis; IEA.

DR InterPro; IPR011029; DEATH_like.

DR InterPro; IPR001875; DED.

DR InterPro; IPR001309; ICE_p20.

```
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF01335; DED; 2.
DR SMART; SM00115; CASc; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR PROSITE; PS0168; DED; 2.
SQ SEQUENCE 481 AA; 54874 MW; 433807E2E5FA5A05 CRC64;

Query Match          56.6%; Score 1018; DB 2; Length 481;
Best Local Similarity 62.6%; Pred. No. 8.6e-65;
Matches 211; Conservative 41; Mismatches 67; Indels 18; Gaps 5;

QY 1 MAEIGEDLKDSDVSSIFLMKQVMGKSIKEKSFLLDLVLEKLNVLAPDQLDLLEKCL 60
DB LMEIGESLDQNDVSSLVFLTRDTGRGKTAKDKSFLLDLVLEKLNLIASDQLNLEKCL 161

QY 61 KNHTRDLTKTKYKQSQVGAGTSRVNLQAAIQ-SLKDPS---NNFREP----- 109
DB KNHTRIDLNTKIQKYTQSSQGA-RSNMNTLQASLPKLSIKYNSRLQNGRSKEPRFVEYRD 220

QY 110 -----VKKGIQSEAFPOSIPERYKMKSPKLGICLIIDICIGNETELLRDFTSLGYEV 164
DB SQTLLVKTSGIQSGAFLPHIREETRYMQSKPLGICLIIDICIGNDKYLOETFTSLGYHI 280

QY 165 QKFLHLSMHGIIQILGQFACMPHEHYDYSFVCLVSRGSGSQSYGVGDQTHSGLPLHHIRR 224
DB QLFLFPKSHDITQIVRRYASMAHQDYDSFACVLSLGGSQSMGGRDQVHSGFSLDHVKN 340

QY 225 MFMGDSCPVLAKPKMFFTONYVSDGLEDSLSLEVDGPMKNVFEKAKGKGLCTVHRE 284
DB MFTGDTCPSLRGKPKLFFTONYESLGSLQEDSS-LEVDPGFSIKNVDSKLPQPRHCTTHPE 399

QY 285 ADFFWSLCTADMSLLPQSSPSLSYLQCLSKLQKQR 321
DB ADFFWSLCTADVSHLEKXPSSSSSVYLQKLSQQLKQR 436

RESULT 4
CFLA_MOUSE
ID CFLA_MOUSE STANDARD; PRT; 484 AA.
AC 035732; 035707; 035733;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE CASP8 and FADD-like apoptosis regulator precursor (Cellular FLICE-like
DE inhibitory protein) (c-FLIP) (Caspase-eight-related protein) (Casper)
DE (Caspase-like apoptosis regulatory protein) (CLARP) (MACH-related
DE inducer of toxicity) (MRT) (Caspase homolog) (CASH) (inhibitor of
DE FLICE) (I-FLICE) (FADD-like antiapoptotic molecule 1) (Flame-1)
DE (Usurpin).
GN Name=Cflar; Synonyms=Cash;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Liver;
RX MEDLINE=97426025; PubMed=9289491; DOI=10.1074/jbc.272.32.19641;
RA Goltsev Y.V., Kovalenko A.V., Arnold E., Varfolomeev E.E.,
RA Brodianskii V.M., Wallach D.;
RT "CASH, a novel caspase homologue with death effector domains.";
RL J. Biol. Chem. 272:19641-19644(1997).
RN [2]
SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Heart;
RX MEDLINE=97360133; PubMed=9217161; DOI=10.1038/40657;
RA Irmier M., Thome M., Hahne M., Schneider P., Hofmann K., Steiner V.,
RA Bodmer J.-L., Schroeter M., Burns K., Mattmann C., Rimoldi D.,
RA French L.E., Tschoep J.;
RT "Inhibition of death receptor signals by cellular FLIP.";
RL Nature 388:190-195(1997).
RN [3]

RP FUNCTION.
RX MEDLINE=20350661; PubMed=10894163; DOI=10.1016/S1074-7613(00)80214-9;
RA Yeh W.-C., Itie A., Elia A.J., Ng M., Shu H.-B., Wakeham A.,
RA Mirzios C., Suzuki N., Bonnard M., Goeddel D.V., Mak T.W.;
RT "Requirement for Casper (c-FLIP) in regulation of death receptor-
induced apoptosis and embryonic development.";
RL Immunity 12:633-642(2000).
RN [4]

RP FUNCTION.
RX MEDLINE=20069388; PubMed=10602037;
RX DOI=10.1002/1521-4141(200001)30:1<155::AID-IMMU155>3.3.CO;2-O;
RA Wang J., Lobito A.A., Shen F., Hornung F., Winoto A., Lenardo M.J.;
RT "Inhibition of Fas-mediated apoptosis by the B cell antigen receptor
through c-FLIP.";
RL Eur. J. Immunol. 30:155-163(2000).
CC -!- FUNCTION: Apoptosis regulator protein which may function as a
crucial link between cell survival and cell death pathways in
mammalian cells. Acts as an inhibitor of TNFRSF6 mediated
apoptosis. A proteolytic fragment (p43) is likely retained in the
death-inducing signaling complex (DISC) thereby blocking further
recruitment and processing of caspase-8 at the complex. Full
length and shorter isoforms have been shown either to induce
apoptosis or to reduce TNFRSF-triggered apoptosis. Lacks enzymatic
(caspase) activity (By similarity).
CC -!- SUBUNIT: TNFRSF6 stimulation triggers recruitment to the death-
inducing signaling complex (DISC) formed by TNFRSF6, FADD and
caspase-8. A proteolytic fragment (p43) stays associated with the
DISC (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=FLIP-L, CASH alpha;
IsoId=O35732-1; Sequence=Displayed;
Name=2; Synonyms=FLIP-S, CASH beta;
IsoId=O35732-2; Sequence=VSP_000842, VSP_000843;
CC -!- TISSUE SPECIFICITY: Highly expressed in heart.
CC -!- DEVELOPMENTAL STAGE: At embryonic days E9.5 and E10.5 highest
expression in developing heart.
CC -!- INDUCTION: Isoform 1 but not isoform 2 is activated by BCR cross-
linking in primary B-cells.
CC -!- DOMAIN: The caspase domain lacks the active sites residues
involved in catalysis.
CC -!- PTM: Proteolytically processed; probably by caspase-8. Processing
likely occurs at the DISC, generates subunit p43 and p12 (By
similarity).
CC -!- SIMILARITY: Belongs to the peptidase C14 family.
CC -!- SIMILARITY: Contains 2 death effector (DED) domains.
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or send an email to license@isb-sib.ch).
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EMBL; Y14041; CAA74368.1; -.
DR EMBL; Y14042; CAA74369.1; -.
DR EMBL; U97076; AAC53281.1; -.
DR HSSP; Q9C0K4; IQTN.
DR MEROPS; C14.974; -.
DR MGD; MGI:1336166; Cflar.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001875; DED.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF01335; DED; 2.
DR Pfam; PF00656; Peptidase C14; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR PROSITE; PS0168; DED; 2.
KW Alternative splicing; Apoptosis; Repeat.
CHAIN 1 380 CASP8 and FADD-like apoptosis regulator
subunit p43 (By similarity).
CHAIN 381 484 CASP8 and FADD-like apoptosis regulator
subunit p12 (By similarity).
FT
FT
```



```
Q8UVG5
ID Q8UVG5 PRELIMINARY; PRT; 418 AA.
AC Q8UVG5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Clarp1.
GN Name=clarp;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98021435; PubMed=9380701; DOI=10.1073/pnas.94.20.10717;
RA Inohara N., Koseki T., Hu Y., Chen S., Nunez G.;
RT "CLARP, a death effector domain-containing protein interacts with
RT caspase-8 and regulates apoptosis."
RL Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish."
RL Cell Death Differ. 7:509-510(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448261; AAL41007.1; -.
DR HSSP; P55210; 1140.
DR ZFIN; ZDB-GENE-030826-3; clarp.
DR GO; GO:003693; F:caspase activity; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR Pfam; PF01335; DED; 2.
DR SMART; SM00115; CASP; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS02008; CASPASE_P20; 1.
DR PROSITE; PS0168; DED; 2.
SQ SEQUENCE 418 AA; 47618 MW; C2ECB3AE571E0237 CRC64;

Query Match 26.2%; Score 471; DB 2; Length 418;
Best Local Similarity 34.2%; Pred. No. 1.4e-25;
Matches 118; Conservative 59; Mismatches 102; Indels 66; Gaps 11;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKSEKSFLLDVVELEKLNVLVAPDQDLLEKCL 60
||:|||||:|||||: : : : : |||||: : : |||||: : : |||||
Db 106 MADVSENLDKEDLQSLIFLLSSILPKERSTRATSFLLDVVELEKLNVEKCLDFLEKCL 165

QY 61 KNHRIIDLTKTKQYKQSQVGAGTSYRNVLQAAIQSKLNDPSNFPREPVKKSIOESEAF 120
||:|||||:|||||: : : : : |||||: : : |||||: : : |||||
Db 166 KNIRNDLVKKIQAYRNQNNPCAAAPNTFKFTPMQC-----QPFKQVRSQCF 215

QY 121 -----LPOSIEP-----ERYKMSKPLGICLIIDICIGNETELLARDFTSLGY-- 162
||:|||||:|||||: : : : : |||||: : : |||||: : : |||||
Db 216 NHEFNKLIKLVETPGTHYQQAITEEYQMPNPEQRLCVIIDCVGYDGEMLKHTFECLGFKV 275

QY 163 -----EVQKFLH-LSMHGITSQILGQFACMPHERDYDSFVCLVSRGGSQSVYGVQ 212
||:|||||:|||||: : : : : |||||: : : |||||: : : |||||
Db 276 VFHSLILGLKETQKVEDLS--LNRILQVRVC-----FVCLISRGTNTHLLATDS 323

QY 213 THSGPLPHHIRMFMGDSCPYLAKGPKMFFIQNYVVSQDGL---EDSSILLEVDGPKMKV 269
||:|||||:|||||: : : : : |||||: : : |||||: : : |||||
Db 324 NRLGINLKDQLFNATKC-----PKIFFTQLYRITAEAPVMPMSMDLEYLETDA PASR-- 375

QY 270 EFKAQRGLCTVHREADFFWSLCTADMSLLEQSHSPSLVLOCLS 314
||:|||||:|||||: : : : : |||||: : : |||||: : : |||||
Db 376 ----QCSGTGVPMPADVLWSVCTAEVKLEES-GHQSVILNALN 415
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RESULT 7
Q6QN98
ID Q6QN98 PRELIMINARY; PRT; 219 AA.
AC Q6QN98;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cellular FLICR-like inhibitory protein short form.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Goto Y., Maeda A., Matsuda F., Inoue N., Manabe N.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY533020; AAS22336.1; -.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR011029; DEATH_Like.
DR InterPro; IPR001875; DED.
DR Pfam; PF01335; DED; 2.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS0168; DED; 2.
SQ SEQUENCE 219 AA; 25303 MW; 840DC7135D88AAC8 CRC64;

Query Match 22.4%; Score 403.5; DB 2; Length 219;
Best Local Similarity 75.7%; Pred. No. 4.2e-21;
Matches 81; Conservative 12; Mismatches 13; Indels 1; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKSEKSFLLDVVELEKLNVLVAPDQDLLEKCL 60
||:|||||:|||||: : : : : |||||: : : |||||: : : |||||
Db 102 MMEIGEGLDKSDVSSLIPLMRDHISRSKWAKDKSFLDLVIELEKLNVLVAPDHLDLLEKCL 161

QY 61 KNHRIIDLTKTKQYKQSQVGAGTSYRNVLQAAIQK-SLKDPSNFR 106
||:|||||:|||||: : : : : |||||: : : |||||: : : |||||
Db 162 RNHRIIDLTKTKQYKQSQGAETNYVNALQASLPNLSIKDPSYNLR 208

RESULT 8
Q99MZ5
ID Q99MZ5 PRELIMINARY; PRT; 218 AA.
AC Q99MZ5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE FLIP short form.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22131045; PubMed=12135878;
RA Xiao C.W., Asselin E., Tsang B.K.;
RT "Nuclear factor kappaB-mediated induction of Flice-like inhibitory
RT protein prevents tumor necrosis factor alpha-induced apoptosis in rat
RT granulosa cells."
RL Biol. Reprod. 67:436-441(2002).
DR EMBL; AF244366; AAK28358.1; -.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR011029; DEATH_Like.
DR InterPro; IPR001875; DED.
DR Pfam; PF01335; DED; 2.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS0168; DED; 2.
SQ SEQUENCE 218 AA; 24718 MW; 9DA9EBAF3441967B CRC64;

Query Match 19.2%; Score 345; DB 2; Length 218;
Best Local Similarity 67.3%; Pred. No. 6.7e-17;
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RA Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,
RA Armstrong R.C., Alnemri E.S.;
RT "FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates
RT Fas/TNFR1-induced apoptosis.";
RL J. Biol. Chem. 272:18542-18545 (1997).
RN [16]
RN SEQUENCE FROM N.A.
RX MEDLINE=21100893; PubMed=11161814; DOI=10.1006/geno.2000.6392;
RA Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,
RA Martindale D., Koop B.F., Scher S.W., Nicholson D.W., Rouleau G.A.,
RA Ikeda J.-E., Hayden M.R.;
RT "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,
RT and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
RT critical region at chromosome 2q33-q34: candidate genes for ALS2.";
RL Genomics 71:200-213 (2001).
RN [7]
RN SEQUENCE FROM N.A. (ISOFORM 7), AND FUNCTION OF ISOFORM 7.
RP TISSUE=Leukocyte;
RX MEDLINE=22005982; PubMed=12010809; DOI=10.1182/blood.V99.11.4070;
RA Himeji D., Horiuchi T., Tsukamoto H., Hayashi K., Watanabe T.,
RA Harada M.;
RT "Characterization of caspase-8L: a novel isoform of caspase-8 that
RT behaves as an inhibitor of the caspase cascade.";
RL Blood 99:4070-4078 (2002).
RN [8]
RN SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 9), AND INTERACTION OF ISOFORM 9
RP WITH BCAP31 AT THE ENDOPLASMIC RETICULUM.
RX MEDLINE=21927603; PubMed=11917123; DOI=10.1073/pnas.072088099;
RA Breckenridge D.G., Nguyen M., Kuppig S., Reth M., Shore G.C.;
RT "The procaspase-8 isoform, procaspase-8L, recruited to the BAP31
RT complex at the endoplasmic reticulum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4331-4336 (2002).
RN [9]
RN SEQUENCE FROM N.A. (ISOFORM 7).
RP TISSUE=Leukocyte;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinaki M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [10]
RN PARTIAL SEQUENCE, AND PROCESSING.
RX MEDLINE=97121412; PubMed=8962078; DOI=10.1073/pnas.93.25.14486;
RA Alnemri E.S.;
RA Alnemri E.S.;
RT "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1
RT protease Mch5 is a CrmA-inhibitable protease that activates multiple
RT Ced-3/ICE-like cysteine proteases.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491 (1996).
RN [11]
RN FUNCTION.
RX MEDLINE=97160607; PubMed=9006941; DOI=10.1074/jbc.272.5.2952;
RA Muzio M., Salvesen G.S., Dixit V.M.;
RT "FLICE induced apoptosis in a cell-free system. Cleavage of caspase
RT zymogens.";
RL J. Biol. Chem. 272:2952-2956 (1997).
RN [12]
RN PROCESSING.
RX MEDLINE=97327557; PubMed=9184224; DOI=10.1093/emboj/16.10.2794;
RA Medema J.P., Scaffidi C., Kischkel F.C., Shevchenko A., Mann M.,
RA Kramer P.H., Peter M.E.;
RT "FLICE is activated by association with the CD95 death-inducing
RT signaling complex (DISC).";
RL EMBO J. 16:2794-2804 (1997).
RN [13]
RN CHARACTERIZATION OF ISOFORM 7.
RX MEDLINE=20318377; PubMed=10860845; DOI=10.1006/bbrc.2000.2841;
RA Horiuchi T., Himeji D., Tsukamoto H., Harashima S., Hashimura C.,
RA Hayashi K.;
RT "Dominant expression of a novel splice variant of caspase-8 in human
RT peripheral blood lymphocytes.";
RL Biochem. Biophys. Res. Commun. 272:877-881 (2000).
RN [14]
RN INTERACTIONS WITH BCL2; BCL2L1 AND BCAP31.
RX MEDLINE=97477382; PubMed=9334338; DOI=10.1083/jcb.139.2.327;
RA Ng F.W.H., Nguyen M., Kwan T., Branton P.E., Nicholson D.W.,
RA Cromlish J.A., Shore G.C.;
RT "p28 Bap31, a Bcl-2/Bcl-XL- and procaspase-8-associated protein in the
RT endoplasmic reticulum.";
RL J. Cell Biol. 139:327-338 (1997).
RN [15]
RN INTERACTION WITH PEAL5.
RX MEDLINE=99369240; PubMed=1042631; DOI=10.1038/sj.onc.1202831;
RA Condorelli G., Vigliotta G., Cafieri A., Trencia A., Andalo P.,
RA Oriente F., Miele C., Caruso M., Fornisano P., Beguinot F.;
RT "PED/PBA-15: an anti-apoptotic molecule that regulates Fas/TNFR1-
RT induced apoptosis.";
RL Oncogene 18:4409-4415 (1999).
RN [16]
RN SPICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
RA Hillman R.T., Green R.E., Bremner S.E.;
RT "An unappreciated role for RNA surveillance.";
RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16 (2004).
RN [17]
RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=99451259; PubMed=10508784; DOI=10.1016/S0969-2126(99)80179-8;
RA Blanchard H., Kodandapani L., Mittl P.R.E., Di Marco S., Krebs J.F.,
RA Wu J.C., Tomaselli K.J., Gruetter M.G.;
RT "The three-dimensional structure of caspase-8: an initiator enzyme in
RT apoptosis.";
RL Structure 7:1125-1133 (1999).
RN [18]
RN VARIANT CASP8D TRP-248.
RX MEDLINE=22239940; PubMed=12353035; DOI=10.1038/nature01063;
RA Chun H.J., Zheng L., Ahmad M., Wang J., Speirs C.K., Siegel R.M.,
RA Dale J.K., Puck J., Davis J., Hall C.G., Skoda-Smith S.,
RA Atkinson T.P., Straus S.E., Lenardo M.J.;
RT "Pleiotropic defects in lymphocyte activation caused by caspase-8
RT mutations lead to human immunodeficiency.";
RL Nature 419:395-399 (2002).
RN CC -!- FUNCTION: Most upstream protease of the activation cascade of
CC caspases responsible for the TNFRSF6/Fas mediated and TNFRSF1A
CC induced cell death. Binding to the adapter molecule FADD recruits
CC it to either receptor. The resulting aggregate called death-
CC inducing signaling complex (DISC) performs CASP8 proteolytic
CC activation. The active dimeric enzyme is then liberated from the
CC DISC and free to activate downstream apoptotic proteases.
CC Proteolytic fragments of the N-terminal propeptide (termed CAP3,
CC CAP5 and CAP6) are likely retained in the DISC. Cleaves and
CC activates CASP3, CASP4, CASP6, CASP7, CASP9 and CASP10. May
CC participate in the GZMB apoptotic pathways. Cleaves ADPRT.
CC Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-|-AMC.
CC Isoforms 5, 6, 7 and 8 lack the catalytic site and may interfere
CC with the pro-apoptotic activity of the complex.
CC -!- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 10 kDa (p10) subunit.
CC Interacts with FADD, CFLAR and PEAL5. Isoform 9 interacts at the
CC endoplasmic reticulum with a complex containing BCAP31, BAP29,
CC BCL2 and/or BCL2L1.


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Query Match 15.4%; Score 277; DB 2; Length 78;
Best Local Similarity 73.1%; Pred. No. 1.4e-12;
Matches 57; Conservative 2; Mismatches 1; Indels 18; Gaps 1;

QY 86 YRNVLAQAQKSLKDPNNPFR-----EPPVKGIQSEAFLPQSIPE 127
Db 1 YKNVLAQAQKSLKDPNNPFRNLHNGRSKEORLKEQLGTQEPVKTIQSEAFLPQSIPE 60

QY 128 ERYKMSKPLGICLIIDC 145
Db 61 ERYKMSKPLGICLIIDC 78

RESULT 14
ID Q6PAD9 PRELIMINARY; PRT; 512 AA.
AC Q6PAD9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC68465 protein.
GN Name=MGC68465;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the peptidase C14 family.
DR EMBL; BC060356; AAH60356.1; -.
DR HSSP; P55210; 1K86.
DR GO; GO:0030693; F:casein activity; IEA.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
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DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF01335; DED_2.
DR PRINTS; PR00376; IL1BCENZYME.
DR SMART; SM00115; CASC; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR PROSITE; PS0168; DED; 2.
KW Hydrolase; Protease; Thiol protease; Zymogen.
SQ SEQUENCE 512 AA; 58799 MW; FE91F00AD8C0EFBB CRC64;

Query Match 15.0%; Score 270; DB 2; Length 512;
Best Local Similarity 27.5%; Pred. No. 4.7e-11;
Matches 100; Conservative 55; Mismatches 142; Indels 66; Gaps 14;

QY 3 EIGEDLDKDVSSLIPLMKDYMGKGIKSEKSFLLDLVBLEKLNLVAPDQDLLEKLN 62
Db 104 EISENTGDDKRIILFLP---FQKHKNKTFDLVLCLEKENSITDNVGLLEDFK 160
QY 63 IHRIDLTKIKYKQ---SVQ-GAGTSYRNVL---QAAIQSKLKDPNSN----- 103
Db 161 VSP-DLLKTIKYKERENNLQPSAPPEYEHLELNPPLSIQVSSKNESWNEETDLIEH 219
QY 104 -NPREPVK-----SIQSEAFLPQ-SIPEERYKMSKPLGICLIID-----C 145
Db 220 GTIHEAEKEDDKSGNIDQLDLRLNPITPOASLMELYDMNRKRGVCLIIDNSIFA 279
QY 146 IGNETS-----LIRDFTSLGYEQKFLHLSMHGISQILGQFACWPEHRDYDSFVCVL 198
Db 280 KGKRGSGDKAGALRDVFNGLDVEIVENLGSEIRDRIKFK-SKHSEKDCVCCI 338
QY 199 VSRGSGSYGVVDQTHSGPLHHRMFMGDSCPYLAGPKMFFIQ-----NYVVDGQLE 254
Db 339 LTHGSGTVLGSDEE--VSIREMSYFTPTSCLSLALKPKLFFIQACQGRYTHPSKVE 396
QY 255 DSSLLEVDGPMKNVFEKQKGLCTVHEADFWSLCTADMQLLSQSHSPSLYLQCLS 314
Db 397 ADATVPE-----HKYIVNVKPEADFLGMSTVDGYFAFRHRTGSGWYIQALC 445
QY 315 QKL 317
Db 446 KNL 448

RESULT 15
QY1B62 PRELIMINARY; PRT; 520 AA.
AC QY1B62;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Caspase-10 (Xcaspase-10 protein).
GN Name=xCaspase-10;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209426; PubMed=10744739; DOI=10.1074/jbc.275.14.10484;
RA Nakajima K., Takahashi A., Yaoita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
RT family."
RL J. Biol. Chem. 275:10484-10491(2000).
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: June 20, 2005, 12:43:37 ; Search time 166 Seconds
(without alignments)
810.799 Million cell updates/sec

Title: US-10-713-208-6

Perfect score: 1800

Sequence: 1 MAEIGEDLDKSDVSSLIPLM.....ITKDMHFSSLCILLDVIL 348

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1800	100.0	348	2	AAW69230 I-FLICE-2
2	1800	100.0	348	7	ADA10619 Human inh
3	1800	100.0	348	7	ADF76399 Novel hum
4	1800	100.0	348	8	ADJ96514 Human I-F
5	1800	100.0	348	8	ADRI1316 Human inh
6	1774	98.6	366	2	AAV05788 Human MAC
7	1774	98.6	422	3	AAV67419 Usurpin-b
8	1774	98.6	462	8	ADRI4101 Human NF-
9	1635	90.8	384	2	AAV05791 MRIT alph
10	1635	90.8	480	2	AAW58578 Human FIN
11	1635	90.8	480	2	AAW69715 Human Cas
12	1635	90.8	480	2	AAW69229 I-FLICE-1
13	1635	90.8	480	2	AAW76631 Human CFL
14	1635	90.8	480	2	AAV05787 Human MAC
15	1635	90.8	480	2	AAV57454 Human FLI
16	1635	90.8	480	3	AAV57606 Human apo
17	1635	90.8	480	3	AAV67418 Usurpin-a
18	1635	90.8	480	3	AAV03960 FLICE-lik
19	1635	90.8	480	3	AAV03960 FLICE-lik
20	1635	90.8	480	7	ADA10615 Human inh
21	1635	90.8	480	8	ADJ96510 Human I-F
22	1635	90.8	480	8	ADRI1312 Human inh
23	1635	90.8	491	3	AAV03964 FLIP with
24	1630	90.6	391	4	AAV03960 Human gen
25	1630	90.6	391	4	AAU21591 Novel hum

26	1630	90.6	391	5	ABG78973 Human apo
27	1630	90.6	391	7	ADC46232 Human neo
28	1630	90.6	391	7	AAE39801 Human gen
29	1630	90.6	480	2	AAW78903 Human G1
30	1630	90.6	480	7	ADN95807 Human BEC
31	1630	90.6	480	8	ADP54877 Human PRO
32	1618	89.9	479	2	AAW76625 Human FLI
33	1579	87.7	480	3	AAV59414 Human CLA
34	1579	87.7	480	7	ADJ68469 Human hea
35	1554.5	86.4	445	5	AAE26086 Human FLA
36	1554.5	86.4	445	5	AAE26086 Human FLA
37	1229	68.3	302	2	AAV05792 MRIT-ND1
38	1128	62.7	264	2	AAV05790 Human ant
39	1018	56.6	481	2	AAW76632 Mouse CFL
40	1018	56.6	481	3	AAV03958 FLICE-lik
41	1018	56.6	481	5	ABB09295 Mouse FLI
42	1018	56.6	483	2	AAW76626 Murine FLI
43	1006.5	55.9	484	5	ABB09292 Mouse FLI
44	1006.5	55.9	484	6	ABB99383 Amino aci
45	978	54.3	230	2	AAV05793 MRIT-Bam

ALIGNMENTS

RESULT 1

AAW69230

ID AAW69230 standard; protein; 348 AA.

XX AAW69230;

XX AAW69230;

DT 18-FEB-1999 (first entry)

XX AAW69230;

DE I-FLICE-2 protein.

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

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XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

XX AAW69230;

CC stroke, CNS inflammation, osteoporosis, ischaemia, reperfusion injury,
 CC cell death associated with cardiovascular disease, polycystic kidney
 CC disease, apoptosis of endothelial cells in cardiovascular disease,
 CC degenerative liver disease, multiple sclerosis (MS) and head injury
 CC damage. Antagonists of the polypeptides can be used for treating cancers
 CC (e.g. follicular lymphomas, carcinomas with p53 mutations, hormone-
 CC dependent tumours, and cancers of the breast, ovary, prostate, bone,
 CC liver, lung, pancreas, and spleen), autoimmune disorders (e.g. systemic
 CC lupus erythematosus, immune-related glomerulonephritis, rheumatoid
 CC arthritis) and viral infections (e.g. herpes viruses, pox viruses and
 CC adenoviruses), graft versus host disease, acute disease, acute graft
 CC rejection, and chronic graft rejection. The products can also be used for
 CC detection, diagnosis and drug screening
 XX
 SQ Sequence 348 AA;

Query Match 100.0%; Score 1800; DB 2; Length 348;
 Best Local Similarity 100.0%; Pred. No. 1.7e-171;
 Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVVELEKLNLVAPDQDLDLEKCL 60
 DB 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVVELEKLNLVAPDQDLDLEKCL 60
 QY 61 KNIHRIDLTKIQYKQSVQAGTSYRNVLAQAIQKSLKDPNNFPPEPVKKSIOSEAF 120
 DB 61 KNIHRIDLTKIQYKQSVQAGTSYRNVLAQAIQKSLKDPNNFPPEPVKKSIOSEAF 120
 QY 121 LPOSIPPEERYKMKSPGLGICLIIDICIGNETELLRTFTSLGYEVQKFLHLSMHGISOILG 180
 DB 121 LPOSIPPEERYKMKSPGLGICLIIDICIGNETELLRTFTSLGYEVQKFLHLSMHGISOILG 180
 QY 181 QFACMPPEHRDYSFVCLVSRGSGSVYGVQDTHSGPLPHHRRMPMGDSCPYLACKPKM 240
 DB 181 QFACMPPEHRDYSFVCLVSRGSGSVYGVQDTHSGPLPHHRRMPMGDSCPYLACKPKM 240
 QY 241 FFIQNVVSDGQLEDSSLLVDGPAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSSLE 300
 DB 241 FFIQNVVSDGQLEDSSLLVDGPAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSSLE 300
 QY 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITKSDMHFSSLGICILLDVL 348
 DB 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITKSDMHFSSLGICILLDVL 348

RESULT 2

ADAL0619

ID ADAL0619 standard; protein; 348 AA.

XX AC ADAL0619;

XX DT 06-NOV-2003 (first entry)

XX DE Human inhibitor of FLICE (I-FLICE-2) protein.

XX Human; I-FLICE-2; inhibitor of FLICE; FADD-like ICE;
 KW tumour necrosis factor receptor-1 inhibitor; TNFR-1 inhibitor;
 KW CD-95 induced apoptosis; apoptosis associated disease;
 KW Alzheimer's disease; rheumatoid arthritis; stroke; osteoporosis;
 KW ischaemia; septic shock; degenerative liver disease;
 KW cardiovascular disorder; aberrant cell survival; neurotropic;
 KW antirheumatic; vasotropic; hepatotropic; osteopathic; cardiac;
 KW cerebroprotective; antibacterial; antiarthritic; vasodilator.

XX OS Homo sapiens.

XX PN US2003087339-A1.

XX PD 08-MAY-2003.

XX PF 21-JAN-1998; 98US-00009893.

XX PR 21-JAN-1997; 97US-0034205P.

PR 05-AUG-1997; 97US-0054800P.

XX (NIJ/) NI J.

PA (ROSE/) ROSEN C A.

PA (DIXI/) DIXIT V M.

PA (GENT/) GENTZ R L.

XX (KENN/) KENNY J J.

PI NI J, Rosen CA, Dixit VM, Gentz RL, Kenny JJ;

XX WPI; 2003-576674/54.

DR N-PSDB; ADA10618.

XX

PT New I-FLICE-1 (inhibitor of FLICE 1) or I-FLICE-2 nucleic acids, useful
 PT for treating diseases associated with apoptosis e.g., Alzheimer's
 PT disease, rheumatoid arthritis, stroke, osteoporosis, ischemia or septic
 PT shock.

XX Claim 1; Fig 4A-4C; 48pp; English.

XX

CC The present invention relates to the isolation of novel human I-FLICE-1
 CC (inhibitor of FLICE (FADD-like ICE)) and I-FLICE-2 proteins, and the
 CC polynucleotide sequences encoding them. The I-FLICE-1 and I-FLICE-2
 CC proteins are novel inhibitors of tumour necrosis factor receptor-1 (TNFR-
 CC 1) and CD-95 induced apoptosis. Also disclosed are vectors, host cells
 CC and recombinant methods for producing the I-FLICE proteins. The sequences
 CC and methods are useful for treating diseases associated with apoptosis
 CC e.g. Alzheimer's disease, rheumatoid arthritis, stroke, osteoporosis,
 CC ischaemia, septic shock, degenerative liver disease, and cardiovascular
 CC disorders. They are also useful for diagnosing diseases or disorders
 CC associated with aberrant cell survival in an individual. The present
 CC sequence represents human I-FLICE-2.

XX Sequence 348 AA;

SQ

Query Match 100.0%; Score 1800; DB 7; Length 348;

Best Local Similarity 100.0%; Pred. No. 1.7e-171;

Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVVELEKLNLVAPDQDLDLEKCL 60

DB 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVVELEKLNLVAPDQDLDLEKCL 60

QY 61 KNIHRIDLTKIQYKQSVQAGTSYRNVLAQAIQKSLKDPNNFPPEPVKKSIOSEAF 120

DB 61 KNIHRIDLTKIQYKQSVQAGTSYRNVLAQAIQKSLKDPNNFPPEPVKKSIOSEAF 120

QY 121 LPOSIPPEERYKMKSPGLGICLIIDICIGNETELLRTFTSLGYEVQKFLHLSMHGISOILG 180

DB 121 LPOSIPPEERYKMKSPGLGICLIIDICIGNETELLRTFTSLGYEVQKFLHLSMHGISOILG 180

QY 181 QFACMPPEHRDYSFVCLVSRGSGSVYGVQDTHSGPLPHHRRMPMGDSCPYLACKPKM 240

DB 181 QFACMPPEHRDYSFVCLVSRGSGSVYGVQDTHSGPLPHHRRMPMGDSCPYLACKPKM 240

QY 241 FFIQNVVSDGQLEDSSLLVDGPAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSSLE 300

DB 241 FFIQNVVSDGQLEDSSLLVDGPAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSSLE 300

QY 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITKSDMHFSSLGICILLDVL 348

DB 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITKSDMHFSSLGICILLDVL 348

RESULT 3

ADF76399

ID ADF76399 standard; protein; 348 AA.

XX AC ADF76399;

XX DT 26-FEB-2004 (first entry)

XX DE Novel human secreted and transmembrane protein SeqID 72.

XX human; PRO: membrane bound protein; membrane bound receptor;
KW cell proliferation; cell migration; cell differentiation;
KW mitogenic factor; survival factor; cytotoxic factor;
KW differentiation factor; neurotrophic factor; hormone; cell receptor;
KW receptor-ligand interaction; cytoskeletal; chondrocyte; tumour.
XX
OS Homo sapiens.
XX WO2003072035-A2.
XX 04-SEP-2003.
XX 21-FEB-2003; 2003WO-US005241.
XX 22-FEB-2002; 2002US-0359461P.
XX (GETH) GENENTECH INC.
XX Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;
PI Williams PM, Wood WI, Wu TD;
XX
XX WPI; 2003-721702/68.
XX N-PSDB; ADF76398.
XX New PRO polypeptides, useful for diagnosing and treating an immune
PT related disorder, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
PT diabetes mellitus.
XX
XX Claim 10; SEQ ID NO 72; 918pp; English.
XX
XX This invention relates to novel nucleic acids encoding human PRO secreted
CC and transmembrane proteins. Extracellular proteins play important roles
CC in the formation, differentiation and maintenance of multicellular
CC organisms. The fate of many individual cells (for example proliferation,
CC migration or differentiation) is typically governed by information
CC received from other cells and the immediate environment. The information
CC is often transmitted by secreted polypeptides (for example mitogenic
CC factors, survival factors, cytotoxic factors, differentiation factors,
CC neurotrophic factors and hormones) which are received and interpreted by diverse
CC cell receptors or membrane bound proteins. These membrane bound proteins
CC and receptors may be of use as pharmaceutical and diagnostic agents, such
CC as in the blocking of receptor-ligand interactions. The current invention
CC provides the amino acid sequences of novel human membrane bound receptors
CC and proteins, along with the cDNA sequences encoding them. The novel
CC proteins of the invention may have cytostatic activities through the
CC stimulation of chondrocytes. The nucleic acids of the invention may be
CC useful for the manufacture of a medicament for diagnosing or treating a
CC tumour in a mammal. In addition, they may be useful for measuring or
CC detecting the expression of a tumour associated gene. The present
CC sequence is the amino acid sequence of a human PRO protein of the
XX invention.
XX
XX Sequence 348 AA;
Query Match 100.0%; Score 1800; DB 7; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.7e-171;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEIGEDLDKSDVSSIFLMKDMYGRGKISKEKSFLLDVLVELEKLNLPADQDLLEKCL 60
DB 1 MAEIGEDLDKSDVSSIFLMKDMYGRGKISKEKSFLLDVLVELEKLNLPADQDLLEKCL 60
QY 61 KNHRIIDLTKIKYKQSVGAGTSYRNVLQAAIQKSLKDPNPNFPKPKSIQSEAF 120
DB 61 KNHRIIDLTKIKYKQSVGAGTSYRNVLQAAIQKSLKDPNPNFPKPKSIQSEAF 120
QY 121 LPQSIPEERYKMKSKPLGICLLIDICGNETELLARDTFTSLGYEVQKFLHLSMHGISQILG 180
DB 121 LPQSIPEERYKMKSKPLGICLLIDICGNETELLARDTFTSLGYEVQKFLHLSMHGISQILG 180
QY 181 QFACMEHRDYSFVCLVSRGSGSVYGVQDTHSGPLPHHIRMFMGDSFCPLAGKPKM 240

DB 181 QFACMEHRDYSFVCLVSRGSGSVYGVQDTHSGPLPHHIRMFMGDSFCPLAGKPKM 240
QY 241 FFIQNYVSDGQLEDSSLLVDGPAKKNVEFKAQKRGCLCTVHREADFFMSLCTADMSLLE 300
DB 241 FFIQNYVSDGQLEDSSLLVDGPAKKNVEFKAQKRGCLCTVHREADFFMSLCTADMSLLE 300
QY 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITESKDMHFSGLCILLDVL 348
DB 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITESKDMHFSGLCILLDVL 348
RESULT 4
ADJ96514
ID ADJ96514 standard; protein; 348 AA.
XX AC ADJ96514;
XX 06-MAY-2004 (first entry)
XX Human I-FLICE-2 protein from clone HCEBJ50.
XX I-FLICE; FADD-like ICE; apoptosis; Alzheimer's disease;
KW Parkinson's disease; rheumatoid arthritis; septic shock; sepsis; stroke;
KW CNS inflammation; osteoporosis; ischaemia; reperfusion injury;
KW cell death; cardiovascular disease; polycystic kidney disease;
KW liver disease; head injury disease; chromosome mapping; human.
XX Homo sapiens.
XX US6680171-B1.
XX 20-JAN-2004.
XX 21-JAN-2000; 2000US-00489155.
XX 21-JAN-1997; 97US-0034205P.
XX 05-AUG-1997; 97US-0054800P.
XX 21-JAN-1998; 98US-00009893.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (UNMI) UNIV MICHIGAN.
XX PI Ni J, Rosen CA, Dixit VM, Gentz RL, Kenny JJ;
XX WPI; 2004-088563/09.
XX N-PSDB; ADJ96513.
XX New human inhibitor of FADD-like ICE (FLICE) nucleic acids and
PT polypeptides, useful for inhibiting apoptosis for treating e.g.
PT Alzheimer's disease, Parkinson's disease, rheumatoid arthritis, sepsis,
PT ischemia, or stroke.
XX
XX Claim 1; SEQ ID NO 6; 58pp; English.
XX
XX The present invention relates to novel I-FLICE (FADD-like ICE)-1 and I-
FLICE (FADD-like ICE)-2 protein and the polynucleotides encoding them.
XX The invention is useful for inhibiting apoptosis and for therapeutic
XX purposes particularly for the treatment of Alzheimer's disease,
XX Parkinson's disease, rheumatoid arthritis, septic shock, sepsis, stroke,
XX CNS inflammation, osteoporosis, ischaemia, reperfusion injury, cell death
XX associated with cardiovascular disease, polycystic kidney disease,
XX apoptosis of endothelial cells in cardiovascular disease, degenerative
XX liver disease, MS and head injury disease. The invention is also useful
XX in chromosome mapping. The present sequence is human I-FLICE protein.
XX
XX Sequence 348 AA;
Query Match 100.0%; Score 1800; DB 8; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.7e-171;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEIGEDLDKSDVSSIFLMKDMYGRGKISKEKSFLLDVLVELEKLNLPADQDLLEKCL 60

CC	diseases, rheumatoid arthritis, septic shock, sepsis, stroke, CNS inflammation, osteoporosis, or ischaemia. The present sequence represents the amino acid sequence of the human inhibitor of FADD-like ICE-2 (I-FLICE-2) HCEBJ50.
XX	Sequence 348 AA;
SQ	Query Match 100.0%; Score 1800; DB 8; Length 348; Best Local Similarity 100.0%; Pred. No. 1.7e-171; Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKEKSFLDLVVELEKLNLVAPDQLDLEKCL 60
DB	1 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKEKSFLDLVVELEKLNLVAPDQLDLEKCL 60
QY	61 KNTHRIDLTKIKQYKQSVQAGTSYRNVLOAAIOKSLKOPSNFRPEPVKKSIOESEAF 120
DB	61 KNTHRIDLTKIKQYKQSVQAGTSYRNVLOAAIOKSLKOPSNFRPEPVKKSIOESEAF 120
QY	121 LPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDTFTSLGYEQKFLHLSMHGISQILG 180
DB	121 LPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDTFTSLGYEQKFLHLSMHGISQILG 180
QY	181 QFACMPEHRDYSFVCLVSRGSGSVYGVQDTHSGLPLHHIRRMFMGDSCPYLAKPKM 240
DB	181 QFACMPEHRDYSFVCLVSRGSGSVYGVQDTHSGLPLHHIRRMFMGDSCPYLAKPKM 240
QY	241 FFQNYVVSQGLEDSLSLEVDGPMKNVFEKAKRGGLCTVHREADFFWSLCTADMSSLE 300
DB	241 FFQNYVVSQGLEDSLSLEVDGPMKNVFEKAKRGGLCTVHREADFFWSLCTADMSSLE 300
QY	301 QSHSSPSLYLQCLSQKLRQERTIPGSGITESKDMHFSSLCILLDVL 348
DB	301 QSHSSPSLYLQCLSQKLRQERTIPGSGITESKDMHFSSLCILLDVL 348
RESULT 6	
AAV05788	
ID	AAV05788 standard; protein; 366 AA.
XX	AAV05788;
FT	02-AUG-1999 (first entry)
XX	Human MACH related inducer of toxicity MRIT alpha 2.
DE	MRIT alpha 2; MACH related inducer of toxicity; human; apoptosis; anti-apoptotic; cancer; autoimmune disease; angiogenesis; atherosclerosis; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; retinitis pigmentosa; stroke; AIDS; infection; aplastic anaemia; myocardial infarction; therapy.
XX	Homo sapiens.
OS	
XX	Key Location/Qualifiers
FT	Active-site 262..266
XX	WO9918230-A2.
PN	
XX	15-APR-1999.
XX	07-OCT-1998; 98WO-US021132.
XX	07-OCT-1997; 97US-00946226.
PR	(UNIW) UNIV WASHINGTON.
XX	Chaudhary PM;
XX	WPI; 1999-277275/23.
DR	N-PSDB; AAX25509.
XX	Identifying regulators of MACH-related inducer of toxicity.

XX Claim 14; Fig 1G; 78pp; English.

XX The present sequence represents novel human MACH-related inducer of

XX toxicity (MRIT) isoform MRIT alpha 2, a CED-4 homologue. Multiple

XX isoforms of MRIT have been identified, some of which function to induce

XX caspase dependent apoptosis in mammalian cells, e.g. MRIT alpha 1 (see

XX AAY05787) and MRIT beta 1 (see AAY05789), while others have anti-

XX apoptotic activity, e.g. MRIT alpha 2. Selective enhancers and inhibitors

XX of MRIT apoptotic activity can be identified and used to treat diseases

XX mediated by the dysfunction of programmed cell death or proliferation. A

XX cell accumulation disorder such as cancer, autoimmune disease, viral

XX infection, angiogenesis or atherosclerosis is treated by administering an

XX agent that selectively enhances MRIT apoptotic activity, thereby inducing an

XX apoptosis in a subject. A disorder of cell loss, such as a

XX neurodegenerative disorder, including Alzheimer's disease, Parkinson's

XX disease, retinitis pigmentosa, stroke, aplastic anaemia, myocardial

XX infarction or AIDS can be treated by administering an agent that

XX selectively inhibits MRIT apoptotic activity

XX Sequence 366 AA;

Query Match 98.6%; Score 1774; DB 2; Length 366;

Best Local Similarity 94.5%; Pred. No. 7.3e-169;

Matches 346; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKEKSFLLDLVVELEKLNVLAPDQDLLEKCL 60

DB 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKEKSFLLDLVVELEKLNVLAPDQDLLEKCL 60

QY 61 KNIHRIDLTKTKIQYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106

DB 61 KNIHRIDLTKTKIQYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106

QY 107 ----BEPVKKSTQSEAFIPQSIPEERYKMKSKPLGICLIIDICINETELLRTDFTSLGY 162

DB 121 LGAQOEPVKKSTQSEAFIPQSIPEERYKMKSKPLGICLIIDICINETELLRTDFTSLGY 180

QY 163 EVQKFLHLSMHGSIQILGQFACMPHERDYDSFVCLVSRGSGSQSVGVVDQTHSGPLPHHI 222

DB 181 EVQKFLHLSMHGSIQILGQFACMPHERDYDSFVCLVSRGSGSQSVGVVDQTHSGPLPHHI 240

QY 223 RRMFGDSCPYLAGPKMFFIQNYVVSQGLDSSSLLLEVDGPKMKVFEKAKRGGLCTVH 282

DB 241 RRMFGDSCPYLAGPKMFFIQNYVVSQGLDSSSLLLEVDGPKMKVFEKAKRGGLCTVH 300

QY 283 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQERGTIPGSGITESKDMHFSSSLGC 342

DB 301 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQERGTIPGSGITESKDMHFSSSLGC 360

QY 343 ILLDVL 348

DB 361 ILLDVL 366

RESULT 7

AAY67419

ID AAY67419 standard; protein; 462 AA.

XX AAY67419;

XX AAY67419;

XX 12-MAY-2000 (first entry)

XX Usurpin-beta polypeptide.

XX Usurpin-alpha; death effector domain; DED; prodomain; usurpin-beta;

XX usurpin-gamma; procaspase-8; CD95; apoptosis; cancer; immunosuppressive;

XX caspase; cytostatic; antiParkinsonian; antidiabetic.

XX Homo sapiens.

XX WO200003023-A1.

XX

PD 20-JAN-2000.

XX 07-JUL-1999; 99WO-CA000615.

XX 08-JUL-1998; 98US-0092005P.

XX (MERI) MERCK FROSST CANADA INC.

XX Nicholson DW, Rasper DM, Xanthoudakis S, Roy S;

XX WPI; 2000-160929/14.

XX N-PSDB; AA256988.

XX Novel recombinant DNA molecules and polypeptides for treating apoptosis

XX mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's

XX disease.

XX Claim 6; Fig 10B; 69pp; English.

XX The invention provides recombinant nucleic acid molecules encoding

XX usurpin-alpha (lacking the first death effector domain (DED) or its

XX prodomain), usurpin-beta or usurpin-gamma. Usurpin polypeptides are

XX useful for in vitro and in vivo identification of usurpin-procaspase-8

XX interaction inhibitor. Usurpin is useful as modulator of the sensitivity

XX of cells to CD95(Fas/Apo-1) mediated apoptosis. Modulation of apoptosis

XX is useful for treating diseases like autoimmune diabetes, cancer and

XX Parkinson's disease. Activators and inhibitors of usurpin-procaspase-8

XX interaction are also useful for treating various diseases mediated by

XX apoptosis. Usurpin provides an attractive model for modulating caspase

XX activation. Sensitivity of cells bearing CD95(Fas/Apo-1) receptor can be

XX regulated at several levels in the presence of usurpin, conferring

XX resistance to Fas-ligand cell death. The present sequence represents the

XX usurpin-beta polypeptide

XX Sequence 462 AA;

Query Match 98.6%; Score 1774; DB 3; Length 462;

Best Local Similarity 94.5%; Pred. No. 1e-168;

Matches 346; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKEKSFLLDLVVELEKLNVLAPDQDLLEKCL 60

DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKEKSFLLDLVVELEKLNVLAPDQDLLEKCL 156

QY 61 KNIHRIDLTKTKIQYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106

DB 157 KNIHRIDLTKTKIQYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 216

QY 107 ----BEPVKKSTQSEAFIPQSIPEERYKMKSKPLGICLIIDICINETELLRTDFTSLGY 162

DB 217 LGAQOEPVKKSTQSEAFIPQSIPEERYKMKSKPLGICLIIDICINETELLRTDFTSLGY 276

QY 163 EVQKFLHLSMHGSIQILGQFACMPHERDYDSFVCLVSRGSGSQSVGVVDQTHSGPLPHHI 222

DB 277 EVQKFLHLSMHGSIQILGQFACMPHERDYDSFVCLVSRGSGSQSVGVVDQTHSGPLPHHI 336

QY 223 RRMFGDSCPYLAGPKMFFIQNYVVSQGLDSSSLLLEVDGPKMKVFEKAKRGGLCTVH 282

DB 337 RRMFGDSCPYLAGPKMFFIQNYVVSQGLDSSSLLLEVDGPKMKVFEKAKRGGLCTVH 396

QY 283 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQERGTIPGSGITESKDMHFSSSLGC 342

DB 397 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQERGTIPGSGITESKDMHFSSSLGC 456

QY 343 ILLDVL 348

DB 457 ILLDVL 462

RESULT 8

ADRI4101

ID ADRI4101 standard; protein; 462 AA.

XX

AC	ADR14101;	CC	invention. Note: This sequence does not appear in the specification but
XX	21-OCT-2004 (first entry)	CC	was obtained by the indexer from Genbank.
XX		XX	
XX	Human NF-kappaB pathway-associated protein SeqID102.	XX	Sequence 462 AA;
XX		XX	Query Match 98.6%; Score 1774; DB 8; Length 462;
XX	NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;	XX	Best Local Similarity 94.5%; Pred. No. 1e-168;
KW	antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;	XX	Matches 346; Conservative 2; Mismatches 0; Indels 18; Gaps 1;
KW	antiartherosclerotic; immunomodulator; cerebroprotective; vasotropic;		
KW	immunosuppressive; vulnary; gene therapy; immune disorder;		
KW	inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;		
KW	hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;		
KW	hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;		
KW	X-linked anhidrotic ectodermal dysplasia; immunodeficiency;		
KW	viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;		
KW	viral replication; host cell survival; evasion of immune response;		
KW	rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;		
KW	atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;		
KW	autoimmune disorder; hyper immune activity;		
KW	aberrant acute phase response; hypercongenital condition; birth defect;		
KW	neurotic lesion; wound; organ transplant rejection;		
KW	aberrant signal transduction; proliferating disorder; cancer;		
KW	HIV propagation; human.		
XX			
OS	Homo sapiens.		
XX			
XX	WO2004065577-A2.		
XX			
XX	05-AUG-2004.		
XX			
XX	13-JAN-2004; 2004WO-US000798.		
XX			
XX	14-JAN-2003; 2003US-0440068P.		
PR	12-MAY-2003; 2003US-0469757P.		
XX			
XX	(BRIM) BRISTOL-MYERS SQUIBB CO.		
PA			
XX			
PI	Nadler SG, Neubauer MG, Feder JN, Carman J;		
XX			
XX	WPI; 2004-562168/54.		
DR	N-PSDB; ADR14100.		
XX			
XX	New isolated polynucleotides and polypeptides associated with NF-kappaB		
PT	pathway, useful for diagnosing, treating, or preventing disorders or		
PT	diseases associated with NF-kappaB pathway.		
XX			
XX	Claim 6; SEQ ID NO 102; 237pp; English.		
PS			
XX			
CC	This invention relates to the novel association of protein sequences (and		
CC	the genes which encode them) to the NF-kappaB pathway. The invention may		
CC	be useful for the production of compounds with an antiinflammatory,		
CC	cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,		
CC	gastrointestinal-gen, antiasthmatic, antiartherosclerotic,		
CC	immunomodulator, cerebroprotective, vasotropic, immunosuppressive or		
CC	vulnary activity or for gene therapy. The proteins and nucleotides are		
CC	useful for diagnosing, preventing, treating, or ameliorating conditions		
CC	or diseases associated with the NF-kappaB pathway. The condition is an		
CC	immune disorder, an inflammatory disorder, an inflammatory disorder		
CC	related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,		
CC	hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM		
CC	syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic		
CC	ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,		
CC	hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell		
CC	survival, evasion of immune responses, rheumatoid arthritis, inflammatory		
CC	bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick		
CC	syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper		
CC	immune activity, disorders related to aberrant acute phase responses,		
CC	hypercongenital conditions, birth defects, necrotic lesions, wounds,		
CC	organ transplant rejection, conditions related to organ transplant		
CC	rejection, disorders related to aberrant signal transduction,		
CC	proliferating disorders, cancers and HIV propagation in cells infected		
CC	with other viruses. The present sequence is that of a human protein which		
CC	is subject to the novel association with the NF-kappaB pathway of the		

CC	invention. Note: This sequence does not appear in the specification but		
XX	was obtained by the indexer from Genbank.		
XX			
XX	Sequence 462 AA;		
XX			
XX	Query Match 98.6%; Score 1774; DB 8; Length 462;		
XX	Best Local Similarity 94.5%; Pred. No. 1e-168;		
XX	Matches 346; Conservative 2; Mismatches 0; Indels 18; Gaps 1;		
XX			
QY	1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLVVELEKLNLVAPDQLLEKCL 60		
DB	97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLVVELEKLNLVAPDQLLEKCL 156		
QY	61 KNIHRIDLTKTIQKYQSQVAGTSYRNVLQAAIQKSLKDPNSNFR----- 106		
DB	157 KNIHRIDLTKTIQKYQSQVAGTSYRNVLQAAIQKSLKDPNSNFRNLHNGRSKEQRLKEQ 216		
QY	107 ----BEPVKYSQSEAFIPQSIPEERYKMSKPLGICLIIDCIGNETELLDRDTTSLGY 162		
DB	217 LGAQQEPVKYSQSEAFIPQSIPEERYKMSKPLGICLIIDCIGNETELLDRDTTSLGY 276		
QY	163 EVQKFLHLSMHGISQILGQFACMPHEDYDVSFVCLVSRGGSQSVYGVDOHSGPLHHI 222		
DB	277 EVQKFLHLSMHGISQILGQFACMPHEDYDVSFVCLVSRGGSQSVYGVDOHSGPLHHI 336		
QY	223 RRMFMGDCPYLAGPKPMFFIYVYVSDGQLEDSSILLEVDGPMKNVFEKAKRGICLVH 282		
DB	337 RRMFMGDCPYLAGPKPMFFIYVYVSDGQLEDSSILLEVDGPMKNVFEKAKRGICLVH 396		
QY	283 READPFWSLCTADMSLLSQSHSSPSLYLQCLSQKLQERGTIPGSGITESKDMHFSLLGC 342		
DB	397 READPFWSLCTADMSLLSQSHSSPSLYLQCLSQKLQERGTIPGSGITESKDMHFSLLGC 456		
QY	343 ILLDVL 348		
DB	457 ILLDVL 462		
XX			
XX	RESULT 9		
XX	AAAY05791		
XX	ID AAY05791 standard; protein; 384 AA.		
XX	AC AAY05791;		
XX	AC AAY05791;		
XX	DT 02-AUG-1999 (first entry)		
XX	DE MRIT alpha 3 polypeptide.		
XX			
XX	MRIT alpha 3; MACH related inducer of toxicity; human; apoptosis;		
XX	anti-apoptotic; cancer; autoimmune disease; angiogenesis;		
XX	atherosclerosis; neurodegenerative disease; Alzheimer's disease;		
XX	Parkinson's disease; retinitis pigmentosa; stroke; AIDS; infection;		
XX	aplastic anaemia; myocardial infarction; therapy; mutant.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
XX	WO9918230-A2.		
XX			
XX	15-APR-1999.		
XX			
XX	07-OCT-1998; 98WO-US021132.		
XX			
XX	07-OCT-1997; 97US-00946226.		
XX	(UNIW) UNIV WASHINGTON.		
XX	Chaudhary PM;		
XX	WPI; 1999-277275/23.		
XX	Identifying regulators of MACH-related inducer of toxicity.		
XX			

PS Example 2; Page; 78pp; English.

XX The present sequence represents MRIT alpha 3, comprising amino acid

CC residues 97-480 of novel human MACH-related inducer of toxicity MRIT

CC alpha 1 (see AY05787). This deletion mutant was used to examine the

CC interaction of MRIT alpha 1 with caspases. The results indicated that

CC FLICE-p20 binding to MRIT alpha 1 does not require the N-terminal 96

CC amino acids. The invention provides multiple isoforms of MRIT (see

CC AY05787-89), isolated active fragments of which have either pro-

CC apoptotic or anti-apoptotic activity. Selective enhancers and inhibitors

CC of MRIT apoptotic activity can be identified and used to treat diseases

CC mediated by the dysfunction of programmed cell death or proliferation,

CC such as cancer or a neurodegenerative disorder. Note: the present

CC sequence is not shown in the specification but is derived from the MRIT

CC alpha 1 sequence given in figure 1f

XX

SQ Sequence 384 AA;

Query Match 90.8%; Score 1635; DB 2; Length 384;

Best Local Similarity 94.1%; Pred. No. 7.1e-155;

Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSILFLMKDYMGRGKISKESFLDLVVELEKLNVLVAPDQDLLEKCL 60

DB 1 MAEIGEDLDKSDVSSILFLMKDYMGRGKISKESFLDLVVELEKLNVLVAPDQDLLEKCL 60

QY 61 KNIHRIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106

DB 61 KNIHRIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106

QY 107 ----EPPVKKSTQESFAFLPQSIPEERYKMKSPKPGICLIIDICIGNETELLRTFTSLGY 162

DB 121 LGAQQEPVKKSTQESFAFLPQSIPEERYKMKSPKPGICLIIDICIGNETELLRTFTSLGY 180

QY 163 EVQKFLHLSMHGISOILGQFACMPHEHDYDSFVCLVSRGGSQSVGVVDQTHSGPLPHHI 222

DB 181 EVQKFLHLSMHGISOILGQFACMPHEHDYDSFVCLVSRGGSQSVGVVDQTHSGPLPHHI 240

QY 223 RRMFMGDCSPYLAGPKPMFFIQNYVVDGQLEDSSLLVEDGPMKNVFEKAKRGGLCTVH 282

DB 241 RRMFMGDCSPYLAGPKPMFFIQNYVVDGQLEDSSLLVEDGPMKNVFEKAKRGGLCTVH 300

QY 283 READPFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 321

DB 301 READPFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 339

RESULT 10

AAW58578

ID AAW58578 standard; protein; 480 AA.

AC AAW58578;

XX 07-SEP-1998 (first entry)

XX Human FIN-1.

DE Human; FIN-1; FLICE inhibitor-1; ICE-LAP7; death effector domain; DEB;

XX apoptosis-related protein; caspase; viral infection; cancer; tumour;

KW diagnosis; ischaemic injury; neuro-degenerative disorder.

XX Homo sapiens.

XX EP841399-A2.

XX 13-MAY-1998.

XX 10-NOV-1997; 97EP-00309003.

XX 12-NOV-1996; 96US-00748086.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX

PI Kikly K, Emery JG;

XX WPI; 1998-252943/23.

DR N-PSDB; AAV311375.

XX New nucleic acid encoding human apoptosis-related protein - used for

PT diagnosis and treatment of e.g. viral infections, tumour, ischaemic

PT injury and neuro-degenerative disorders.

XX Claim 11; Page 25-27; 48pp; English.

XX The present sequence represents human FIN-1 (FLICE inhibitor-1), which is

CC a caspase. FLICE (ICE-LAP7) is a protease of the interleukin-converting

CC enzyme family, a protein involved in the regulation of cell death. A host

CC cell, comprising a vector containing the FIN-1 encoding DNA, can be used to

CC produce FIN-1. The vector contains the DNA can be used for producing a

CC cell which expresses a polypeptide by transforming or transfecting the

CC cell with it so that the cell expresses the polypeptide encoded the human

CC cDNA contained in the vector. The polypeptide or its antagonist can be

CC used in the treatment of patients needing FIN-1 by in-vivo

CC administration. Conditions which may be treated include viral infection,

CC tumours (especially solid tumours), ischaemic injury (e.g. stroke or

CC myocardial infarction), neurodegenerative disorders (e.g. Alzheimer's or

CC Parkinson's disease), osteoporosis, osteoarthritis, polycystic kidney

CC disease, chronic degenerative liver disease, acquired immunodeficiency

CC syndrome (AIDS) and aplastic anaemia. The polynucleotides may also be

CC used for chromosome identification

XX

SQ Sequence 480 AA;

Query Match 90.8%; Score 1635; DB 2; Length 480;

Best Local Similarity 94.1%; Pred. No. 9.9e-155;

Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSILFLMKDYMGRGKISKESFLDLVVELEKLNVLVAPDQDLLEKCL 60

DB 97 MAEIGEDLDKSDVSSILFLMKDYMGRGKISKESFLDLVVELEKLNVLVAPDQDLLEKCL 156

QY 61 KNIHRIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106

DB 157 KNIHRIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPNNFR----- 216

QY 107 ----EPPVKKSTQESFAFLPQSIPEERYKMKSPKPGICLIIDICIGNETELLRTFTSLGY 162

DB 217 LGAQQEPVKKSTQESFAFLPQSIPEERYKMKSPKPGICLIIDICIGNETELLRTFTSLGY 276

QY 163 EVQKFLHLSMHGISOILGQFACMPHEHDYDSFVCLVSRGGSQSVGVVDQTHSGPLPHHI 222

DB 277 EVQKFLHLSMHGISOILGQFACMPHEHDYDSFVCLVSRGGSQSVGVVDQTHSGPLPHHI 336

QY 223 RRMFMGDCSPYLAGPKPMFFIQNYVVDGQLEDSSLLVEDGPMKNVFEKAKRGGLCTVH 282

DB 337 RRMFMGDCSPYLAGPKPMFFIQNYVVDGQLEDSSLLVEDGPMKNVFEKAKRGGLCTVH 396

QY 283 READPFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 321

DB 397 READPFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 435

RESULT 11

AAW69715

ID AAW69715 standard; protein; 480 AA.

AC AAW69715;

XX 24-NOV-1998 (first entry)

XX Human Casper protein.

DE Casper; caspase-eight-related protein; human; apoptosis.

XX Homo sapiens.

XX

PN WO9833883-A1.
XX
PD 06-AUG-1998.
XX
XX 05-FEB-1998; 98WO-US002117.
PF
XX 05-FEB-1997; 97US-00795088.
PR
XX (TULA-) TULARIK INC.
PA
XX Shu H, Goeddel DV;
PI
XX WPI; 1998-437440/37.
DR
XX N-PSDB; AAV50436.
DR
XX
PT New Casper protein involved in regulation of apoptosis - used, e.g. to
PT identify specific modulators, identify or isolate similar sequences and
PT in gene therapy.
XX
XX
PS Claim 1; Page 22-23; 29pp; English.
XX
XX This is the amino acid sequence of a novel human protein, designated
CC Casper (for caspase-eight-related protein), that is involved in
CC regulation of apoptosis. The sequence is deduced from an isolated cDNA
CC clone (see AAV50436). Casper protein interacts with FADD and is recruited
CC to Fas. It also interacts with caspase-8 and caspase-3, and with TRAF1
CC and TRAF2. A claimed isolated polypeptide comprises the full-length
CC Casper amino acid sequence, or a fragment of at least 6 consecutive amino
CC acid residues including at least one of residues 1-96, 1-202, 1-435, 78-
CC 480, 192-480, 390-480 or residue 360. The isolated protein, or cells that
CC express the protein, can be used to screen for agents, e.g. antibodies or
CC T-cell receptors, that specifically modify the binding of Casper to a
CC target, and thus its function
XX
XX Sequence 480 AA;
SQ

Query Match 90.8%; Score 1635; DB 2; Length 480;
Best Local Similarity 94.1%; Pred. No. 9.9e-155;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKESFLDLVVELEKLNLVAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKESFLDLVVELEKLNLVAPDQDLLEKCL 156

QY 61 KNHRIIDLTKTKQYKQSVQAGTGYRNVLQAAIQKSLKDPNNFR----- 106
DB 157 KNHRIIDLTKTKQYKQSVQAGTGYRNVLQAAIQKSLKDPNNFHLNGRSKEQRLKEQ 216

QY 107 -----EPPVKKSIOESEAFIPQSIPEERYKMKSKPLGICLIIDICIGNETELLRDFTTSLGY 162
DB 217 LGAQQEPVKKSIOESEAFIPQSIPEERYKMKSKPLGICLIIDICIGNETELLRDFTTSLGY 276

QY 163 EVQKFLHLSMHGISOILGQFACMPERHDYDSFVCLVSRGSGSVYGVQDTHSGPLHHI 222
DB 277 EVQKFLHLSMHGISOILGQFACMPERHDYDSFVCLVSRGSGSVYGVQDTHSGPLHHI 336

QY 223 RRMFMGDSCPYLAGKPKMFIFQYNYVSDGLEDSLSLEVDGPMKNVEFKAQKRGICLVH 282
DB 337 RRMFMGDSCPYLAGKPKMFIFQYNYVSEGLEDSLSLEVDGPMKNVEFKAQKRGICLVH 396

QY 283 READPFWSLCTADMSLLEQSHSPPSYLQCLSQKLQER 321
DB 397 READPFWSLCTADMSLLEQSHSPPSYLQCLSQKLQER 435

RESULT 12
ID AAW69229
XX AAW69229 standard; protein; 480 AA.
AC
XX AAW69229;
XX
DT 16-OCT-1998 (first entry)
XX

DE I-FLICE-1 protein.
XX
KW I-FLICE-1; FADD like ICE protein; inhibitor; TNFR-1; Alzheimer's disease;
KW CD-95 induced apoptosis; Parkinson's disease; rheumatoid arthritis;
KW CNS inflammation; osteoporosis; ischaemia; polycystic kidney disease;
KW multiple sclerosis; head injury; cancer; autoimmune disorder; therapy;
KW viral infection; graft versus host disease; graft rejection.
XX
OS Homo sapiens.
XX
PN WO9831801-A1.
XX
PD 23-JUL-1998.
XX
XX 21-JAN-1998; 98WO-US000969.
PF
XX 21-JAN-1997; 97US-0034205P.
PR
XX 05-AUG-1997; 97US-0054800P.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX (UNMI) UNIV MICHIGAN.
PA
XX Ni J, Rosen CA, Dixit VM, Gentz RL, Kenny JJ;
PI
XX WPI; 1998-414100/35.
DR
XX N-PSDB; AAV44806.
DR
XX
PT New inhibitory polypeptides of FLICE - used to develop products for
PT treating e.g. Alzheimer's disease, sepsis, stroke, osteoporosis, cancers,
PT autoimmune disorders, viral infection or graft rejection.
XX
XX Claim 9; Fig 1; 118pp; English.
XX
XX This sequence is an inhibitor of Fas-ligand associated with death
CC domain (FADD) like ICE (I-FLICE) protein, designated I-FLICE-1. The
CC proteins can inhibit both TNFR-1 and CD-95 induced apoptosis. These are
CC the first examples of a naturally occurring catalytically inactive
CC caspase that can act as a dominant negative inhibitor of apoptosis. The
CC polypeptides and agonists can be used for treating e.g. Alzheimer's
CC disease, Parkinson's disease, rheumatoid arthritis, septic shock, sepsis,
CC stroke, CNS inflammation, osteoporosis, ischaemia, reperfusion injury,
CC cell death associated with cardiovascular disease, polycystic kidney
CC disease, apoptosis of endothelial cells in cardiovascular disease,
CC degenerative liver disease, multiple sclerosis (MS) and head injury
CC (e.g. follicular lymphomas, carcinomas with p53 mutations, hormone-
CC dependent tumours, and cancers of the breast, ovary, prostate, bone,
CC liver, lung, pancreas, and spleen), autoimmune disorders (e.g. systemic
CC lupus erythematosus, immune-related glomerulonephritis, rheumatoid
CC arthritis), and viral infections (e.g. herpes viruses, pox viruses and
CC adenoviruses), graft versus host disease, acute disease, acute graft
CC rejection, and chronic graft rejection. The products can also be used for
CC detection, diagnosis and drug screening
XX
SQ Sequence 480 AA;

Query Match 90.8%; Score 1635; DB 2; Length 480;
Best Local Similarity 94.1%; Pred. No. 9.9e-155;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKESFLDLVVELEKLNLVAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKGKISKESFLDLVVELEKLNLVAPDQDLLEKCL 156

QY 61 KNHRIIDLTKTKQYKQSVQAGTGYRNVLQAAIQKSLKDPNNFR----- 106
DB 157 KNHRIIDLTKTKQYKQSVQAGTGYRNVLQAAIQKSLKDPNNFHLNGRSKEQRLKEQ 216

QY 107 -----EPPVKKSIOESEAFIPQSIPEERYKMKSKPLGICLIIDICIGNETELLRDFTTSLGY 162
DB 217 LGAQQEPVKKSIOESEAFIPQSIPEERYKMKSKPLGICLIIDICIGNETELLRDFTTSLGY 276

QY 163 EVQKFLHLSMHGISOILGQFACMPERHDYDSFVCLVSRGSGSVYGVQDTHSGPLHHI 222
XX


```
Db 277 EVQKFLHLSMHGSIQLGQFACMPHRDYDSFVCVLVSRGSGSVYGVQDTHSGLPLHHI 336
QY 223 RRMFMGDSCPYLAKGPKMPFFIQNYVVSQDQLEDSSLLLEVDGPMKNVFEKAKRGGLCTVH 282
Db 337 RRMFMGDSCPYLAKGPKMPFFIQNYVVSQDQLEDSSLLLEVDGPMKNVFEKAKRGGLCTVH 396
QY 283 READPFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 321
Db 397 READPFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 435

RESULT 14
AAW76631
ID AAW76631 standard; protein; 480 AA.
AC AAW76631;
XX
DT 12-JUL-1999 (first entry)
DE Human CFLIP-L protein.
XX
KW Death effector domain; human; murine; anti-apoptotic; treatment;
KW HIV infection; autoimmune disease; FLIP protein.
XX
OS Homo sapiens.
XX
PN DE19713393-A1.
XX
PD 08-OCT-1998.
XX
PF 01-APR-1997; 97DE-01013393.
XX
PR 01-APR-1997; 97DE-01013393.
XX
PA (TSCH/) TSCHOPP J.
XX
PI Tschopp J, Thome M, Burns K, Irmeler M, Hahne M, Schroeter M;
PI Schneider P, Bodmer J, Steiner V, Rimoldi D, Hoffmann K, French EL;
XX
DR WPI; 1998-532710/46.
DR N-PSDB; AAV61937.
XX
PT New DNA encoding for anti-apoptotic gene product - used to treat HIV
PT infections and autoimmune diseases.
XX
PS Claim 20; Fig 4B; 45pp; German.
XX
CC This invention describes novel human and mouse anti-apoptotic gene
CC products which contain at least one death effector domain. The products
CC of the invention are used in the treatment of HIV infections and
CC autoimmune diseases
XX
SQ Sequence 480 AA;

Query Match 90.8%; Score 1635; DB 2; Length 480;
Best Local Similarity 94.1%; Pred. No. 9.9e-155;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNVLVAPDQDLLEKCL 60
Db 97 MAEIGDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNVLVAPDQDLLEKCL 156
QY 61 KNHRIIDLTKIKYKQSQVQAGTSYRNVLQAAIQSLKDPNNFR----- 106
Db 157 KNHRIIDLTKIKYKQSQVQAGTSYRNVLQAAIQSLKDPNNFNLHNGRSKEQRLKEQ 216
QY 107 -----EPVVKKSQESAFIPQSIPEERYKMKSPGLGICLIIDICIGNETELLDRDTFTSLGY 162
Db 217 LGAQQEPVKKSQESAFIPQSIPEERYKMKSPGLGICLIIDICIGNETELLDRDTFTSLGY 276
QY 163 EVQKFLHLSMHGSIQLGQFACMPHRDYDSFVCVLVSRGSGSVYGVQDTHSGLPLHHI 222
```

```
Db 277 EVQKFLHLSMHGSIQLGQFACMPHRDYDSFVCVLVSRGSGSVYGVQDTHSGLPLHHI 336
QY 223 RRMFMGDSCPYLAKGPKMPFFIQNYVVSQDQLEDSSLLLEVDGPMKNVFEKAKRGGLCTVH 282
Db 337 RRMFMGDSCPYLAKGPKMPFFIQNYVVSQDQLEDSSLLLEVDGPMKNVFEKAKRGGLCTVH 396
QY 283 READPFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 321
Db 397 READPFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQER 435

RESULT 14
AAW05787
ID AAY05787 standard; protein; 480 AA.
AC AAY05787;
XX
DT 02-AUG-1999 (first entry)
DE Human MACH related inducer of toxicity MRIT alpha 1.
XX
KW MRIT alpha 1; MACH related inducer of toxicity; human; apoptosis;
KW pro-apoptotic; cancer; autoimmune disease; infection; angiogenesis;
KW atherosclerosis; neurodegenerative disease; Alzheimer's disease;
KW Parkinson's disease; retinitis pigmentosa; stroke; AIDS;
KW aplastic anaemia; myocardial infarction; therapy.
XX
OS Homo sapiens.
XX
FH Key
FT Region 1..165
FT Region /note= "death effector domain homology region"
FT Region 140..178
FT Region /note= "Bcl-2 homology region"
FT Region 196..228
FT Region /note= "Bcl-2 homology region"
FT Region 258..289
FT Region /note= "Bcl-2 homology region"
FT Region 299..350
FT Region /note= "Bcl-2 homology region"
FT Region 301..480
FT Region /note= "caspase homology region"
FT Region 356..397
FT Active-site /note= "Bcl-2 homology region"
FT 358..362
XX WO9918230-A2.
XX
PD 15-APR-1999.
XX
PF 07-OCT-1998; 98WO-US021132.
XX
PR 07-OCT-1997; 97US-00946226.
XX
PA (UNITW ) UNIV WASHINGTON.
XX
PI Chaudhary PM;
XX
DR WPI; 1999-277275/23.
XX N-PSDB; AAY25508.
XX
PT Identifying regulators of MACH-related inducer of toxicity.
XX
PS Example 1; Fig 1F; 78pp; English.
XX
CC The present sequence represents novel human MACH-related inducer of
CC toxicity (MRIT) isoform MRIT alpha 1, a CED-4 homologue that interacts
CC simultaneously with caspases and Bcl-2 family polypeptides, and which has
CC pro-apoptotic activity. Multiple isoforms of MRIT have been identified,
CC some of which function to induce caspase dependent apoptosis in mammalian
CC cells, e.g. MRIT alpha 1 and MRIT beta 1 (see AAY05789), while others
CC have anti-apoptotic activity, e.g. MRIT alpha 2 (see AAY05788). MRIT
CC alpha 1 includes an N-terminal death effector domain and a C-terminal
```

CC caspase homology domain, but is not a cysteine protease. Selective
CC enhancers and inhibitors of MRIT apoptotic activity can be identified and
CC used to treat diseases mediated by the dysfunction of programmed cell
CC death or proliferation. A cell accumulation disorder such as cancer,
CC autoimmune disease, viral infection, angiogenesis or atherosclerosis is
CC treated by administering an agent that selectively enhances MRIT
CC apoptotic activity, thereby inducing apoptosis in a subject. A disorder
CC of cell loss, such as a neurodegenerative disorder, including Alzheimer's
CC disease, Parkinson's disease, retinitis pigmentosa, stroke, aplastic
CC anaemia, myocardial infarction or AIDS can be treated by administering an
CC agent that selectively inhibits MRIT apoptotic activity

XX Sequence 480 AA;

Query Match 90.8%; Score 1635; DB 2; Length 480;
Best Local Similarity 94.1%; Pred. No. 9.9e-155;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;
QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKEKSFLLDLVVELEKLNVLVAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKEKSFLLDLVVELEKLNVLVAPDQDLLEKCL 156
QY 61 KNIHRIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPNNPR----- 106
DB 157 KNIHRIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPNNPRFLHNGRSKEQRLKEQ 216
QY 107 ----BEPVKKSQESAEFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRDFTTSLGY 162
DB 217 LGAQOEPVKKSQESAEFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRDFTTSLGY 276
QY 163 EVQKFLHLSMHGISQILGQFACMPHEHDYDSFVCLVSRGGSQSVYGVVDQTHSGPLHHI 222
DB 277 EVQKFLHLSMHGISQILGQFACMPHEHDYDSFVCLVSRGGSQSVYGVVDQTHSGPLHHI 336
QY 223 RRMFMGDCPCYLAGKPKMFFIQQYVVSQGLDSSILLEVDGPAMKNVEFKAKRGICLTVH 282
DB 337 RRMFMGDCPCYLAGKPKMFFIQQYVVSQGLDSSILLEVDGPAMKNVEFKAKRGICLTVH 396
QY 283 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLROER 321
DB 397 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLROER 435

RESULT 15
AAY57454
ID AAY57454 standard; protein; 480 AA.
XX AAY57454;
AC AAY57454;

XX 25-FEB-2000 (first entry)
DT Human FLICE-like inhibitory protein long form protein sequence.
DE
DE
XX Human; FLICE-like inhibitory protein long form; FLIP-L; FLIP-S;
XX FLICE-like inhibitory protein short form; apoptosis inhibitor;
KW arteriosclerosis; vascular wall inflammation; vascular injury;
KW Fas ligand-mediated apoptosis; atherosclerosis; transplant.
XX
OS Homo sapiens.

XX
XX WO9942570-A1.
XX
XX 26-AUG-1999.
XX
XX 19-FEB-1999; 99WO-US003558.
XX
XX 20-FEB-1998; 98US-0075471P.
XX
XX (SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.
XX
XX Walsh K;
XX
XX WPI; 1999-527469/44.

DR N-PSDB; AAZ39040.
XX Treating conditions characterized by vascular wall inflammation.
PT
XX
XX Claim 5; Page 69-71; 105pp; English.
PS
XX The present sequence represents human FLICE-like inhibitory protein long
CC form, designated FLIP-L. The present invention describes a new treatment
CC of a condition characterised by vascular wall inflammation in a subject
CC comprising administering a FLIP molecule to inhibit Fas ligand-mediated
CC apoptosis of vascular endothelial cells in the subject. The method can be
CC used to treat atherosclerosis, transplant arteriosclerosis and vascular
CC injury

XX Sequence 480 AA;

Query Match 90.8%; Score 1635; DB 2; Length 480;
Best Local Similarity 94.1%; Pred. No. 9.9e-155;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;
QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKEKSFLLDLVVELEKLNVLVAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKEKSFLLDLVVELEKLNVLVAPDQDLLEKCL 156
QY 61 KNIHRIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPNNPR----- 106
DB 157 KNIHRIDLTKTKQYKQSVQAGTSYRNVLQAAIQKSLKDPNNPRFLHNGRSKEQRLKEQ 216
QY 107 ----BEPVKKSQESAEFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRDFTTSLGY 162
DB 217 LGAQOEPVKKSQESAEFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRDFTTSLGY 276
QY 163 EVQKFLHLSMHGISQILGQFACMPHEHDYDSFVCLVSRGGSQSVYGVVDQTHSGPLHHI 222
DB 277 EVQKFLHLSMHGISQILGQFACMPHEHDYDSFVCLVSRGGSQSVYGVVDQTHSGPLHHI 336
QY 223 RRMFMGDCPCYLAGKPKMFFIQQYVVSQGLDSSILLEVDGPAMKNVEFKAKRGICLTVH 282
DB 337 RRMFMGDCPCYLAGKPKMFFIQQYVVSQGLDSSILLEVDGPAMKNVEFKAKRGICLTVH 396
QY 283 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLROER 321
DB 397 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLROER 435

Search completed: June 20, 2005, 13:02:20
Job time : 170 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2005, 13:02:28 ; Search time 162 Seconds
(without alignments)
824.845 Million cell updates/sec

Title: US-10-713-208-6

Perfect score: 1800

Sequence: 1 MAEIGEDLDKSDVSSILFLM.....ITKDMHFSSIGCILLDVL 348

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1800	100.0	348	10 US-09-009-893-6	Sequence 6, Appli
2	1800	100.0	348	16 US-10-713-208-6	Sequence 6, Appli
3	1800	100.0	348	16 US-10-370-715B-72	Sequence 72, Appli
4	1774	98.6	462	16 US-10-755-889-102	Sequence 102, App
5	1635	90.8	480	9 US-09-861-270-2	Sequence 2, Appli
6	1635	90.8	480	9 US-09-410-194-11	Sequence 11, Appli
7	1635	90.8	480	9 US-09-410-194-17	Sequence 17, Appli
8	1635	90.8	480	10 US-09-009-893-2	Sequence 2, Appli
9	1635	90.8	480	10 US-09-471-749-1	Sequence 1, Appli
10	1635	90.8	480	16 US-10-713-208-2	Sequence 2, Appli
11	1635	90.8	480	17 US-10-832-218-11	Sequence 11, Appli

12	1635	90.8	480	17	US-10-832-218-17	Sequence 17, Appli
13	1630	90.6	391	9	US-09-764-861-37	Sequence 37, Appli
14	1630	90.6	391	10	US-09-764-861-37	Sequence 37, Appli
15	1630	90.6	391	14	US-10-103-313-318	Sequence 318, App
16	1630	90.6	391	14	US-10-115-928-37	Sequence 37, Appli
17	1630	90.6	480	16	US-10-849-901-2	Sequence 2, Appli
18	1579	87.7	480	16	US-10-408-765A-275	Sequence 275, App
19	1554.5	86.4	445	9	US-09-935-223-2	Sequence 2, Appli
20	1554.5	86.4	445	16	US-10-825-282-44	Sequence 44, Appli
21	1018	56.6	481	9	US-09-410-194-12	Sequence 12, Appli
22	1018	56.6	481	17	US-09-410-194-19	Sequence 19, Appli
23	1018	56.6	481	17	US-10-832-218-12	Sequence 12, Appli
24	1018	56.6	481	17	US-10-832-218-19	Sequence 19, Appli
25	1006.5	55.9	484	13	US-10-005-921-2	Sequence 2, Appli
26	1006.5	55.9	484	16	US-10-849-901-5	Sequence 5, Appli
27	527	29.3	221	9	US-09-410-194-15	Sequence 15, Appli
28	527	29.3	221	9	US-09-410-194-22	Sequence 22, Appli
29	527	29.3	221	16	US-10-849-901-4	Sequence 4, Appli
30	527	29.3	221	17	US-10-832-218-15	Sequence 15, Appli
31	527	29.3	221	17	US-10-832-218-22	Sequence 22, Appli
32	391	21.7	76	9	US-09-864-761-35073	Sequence 35073, A
33	313	17.4	479	9	US-09-410-194-20	Sequence 20, Appli
34	313	17.4	479	10	US-09-851-873-101	Sequence 101, App
35	313	17.4	479	15	US-10-368-438-7	Sequence 7, Appli
36	313	17.4	479	16	US-10-849-901-6	Sequence 6, Appli
37	313	17.4	479	17	US-10-832-218-20	Sequence 20, Appli
38	311.5	17.3	478	10	US-09-009-893-3	Sequence 3, Appli
39	311.5	17.3	478	16	US-10-713-208-3	Sequence 3, Appli
40	305.5	17.0	496	16	US-10-825-282-16	Sequence 16, Appli
41	305.5	17.0	496	17	US-10-488-614-8	Sequence 8, Appli
42	305.5	17.0	496	17	US-10-488-608-7	Sequence 7, Appli
43	304.5	16.9	464	15	US-10-368-438-18	Sequence 18, Appli
44	304.5	16.9	496	15	US-10-232-884-6	Sequence 6, Appli
45	302.5	16.8	496	9	US-09-952-768-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-009-893-6

; Sequence 6, Application US/09009893

; Publication No. US20030087339A1

; GENERAL INFORMATION:

; APPLICANT: NI, JIAN

; APPLICANT: ROSEN, CRAIG A.

; APPLICANT: DIXIT, VISHVA M.

; APPLICANT: GENTZ, REINER L.

; APPLICANT: KENNY, JOSEPH J.

; TITLE OF INVENTION: 1-FLICE, A NOVEL INHIBITOR OF TUMOR

; TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APOPTOSIS

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

; STREET: 1100 NEW YORK AVENUE, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: US

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/009,893

; FILING DATE: HEREWITH

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/034,205

; FILING DATE: 21-JAN-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/054,800

FILING DATE: 05-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0970002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-009-893-6

Query Match
Best Local Similarity 100.0%; Score 1800; DB 10; Length 348;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKESKESFLDLVVELEKLNLVAPDQDLDLLEKCL 60
1 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKESKESFLDLVVELEKLNLVAPDQDLDLLEKCL 60
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61 KNIHRIDLTKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNSNFPREPVKKSIQSEAF 120
121 LPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDTFTSLGYEVQKFLHLSMHGSIQILG 180
121 LPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDTFTSLGYEVQKFLHLSMHGSIQILG 180
181 QFACMEPHRDYDSFVCLVSRGGSQSVYGVQDTHSGPLPHHRRMFMGDSFCPLAGKPKM 240
181 QFACMEPHRDYDSFVCLVSRGGSQSVYGVQDTHSGPLPHHRRMFMGDSFCPLAGKPKM 240
241 FFIQNVVSDGQLEDSSLEVDGPAMKNVEFKAQKRGCTVHREADFFWMSLCTADMSSLE 300
241 FFIQNVVSDGQLEDSSLEVDGPAMKNVEFKAQKRGCTVHREADFFWMSLCTADMSSLE 300
301 QSHSSPSLYLQCLSKQLRQERTIPGSGITESKDMHFSSLGICILLDVL 348
301 QSHSSPSLYLQCLSKQLRQERTIPGSGITESKDMHFSSLGICILLDVL 348

RESULT 2
US-10-713-208-6
Sequence 6, Application US/10713208
Publication No. US20040121387A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: I-FLICE, A Novel Inhibitor of Tumor Necrosis Factor Receptor-1 and Induced Apoptosis
FILE REFERENCE: PF381C1D1
CURRENT APPLICATION NUMBER: US/10/713,208
CURRENT FILING DATE: 2003-11-17
PRIOR APPLICATION NUMBER: US 09/489,155
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/009,893
PRIOR FILING DATE: 1998-01-21
PRIOR APPLICATION NUMBER: US 60/054,800
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: US 60/034,205
PRIOR FILING DATE: 1997-01-21
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 348
TYPE: PRT
ORGANISM: Homo sapiens
US-10-713-208-6

Query Match
Best Local Similarity 100.0%; Score 1800; DB 16; Length 348;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 1.4e-160;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKESKESFLDLVVELEKLNLVAPDQDLDLLEKCL 60
1 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKESKESFLDLVVELEKLNLVAPDQDLDLLEKCL 60
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121 LPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDTFTSLGYEVQKFLHLSMHGSIQILG 180
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181 QFACMEPHRDYDSFVCLVSRGGSQSVYGVQDTHSGPLPHHRRMFMGDSFCPLAGKPKM 240
181 QFACMEPHRDYDSFVCLVSRGGSQSVYGVQDTHSGPLPHHRRMFMGDSFCPLAGKPKM 240
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241 FFIQNVVSDGQLEDSSLEVDGPAMKNVEFKAQKRGCTVHREADFFWMSLCTADMSSLE 300
301 QSHSSPSLYLQCLSKQLRQERTIPGSGITESKDMHFSSLGICILLDVL 348
301 QSHSSPSLYLQCLSKQLRQERTIPGSGITESKDMHFSSLGICILLDVL 348

RESULT 3
US-10-370-715B-72
Sequence 72, Application US/10370715B
Publication No. US20040258678A1
GENERAL INFORMATION:
Patent Docket Preview
APPLICANT: BODARY, SARAH C.
APPLICANT: CLARK, HILLARY
APPLICANT: BRISDELL, HUNTE
APPLICANT: JACKMAN, JANET
APPLICANT: SCHOENFELD, JILL R.
APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WOOD, WILLIAM I.
APPLICANT: WU, THOMAS D.
TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
TITLE OF INVENTION: Related Diseases
FILE REFERENCE: P1948R1-US
CURRENT APPLICATION NUMBER: US/10/370,715B
CURRENT FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 742
SEQ ID NO 72
LENGTH: 348
TYPE: PRT
ORGANISM: Homo sapien
US-10-370-715B-72

Query Match
Best Local Similarity 100.0%; Score 1800; DB 16; Length 348;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKESKESFLDLVVELEKLNLVAPDQDLDLLEKCL 60
1 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKESKESFLDLVVELEKLNLVAPDQDLDLLEKCL 60
61 KNIHRIDLTKTKIQKYKQSVQAGTSYRNVLQAAIQKSLKDPNSNFPREPVKKSIQSEAF 120
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121 LPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDTFTSLGYEVQKFLHLSMHGSIQILG 180
121 LPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDTFTSLGYEVQKFLHLSMHGSIQILG 180
181 QFACMEPHRDYDSFVCLVSRGGSQSVYGVQDTHSGPLPHHRRMFMGDSFCPLAGKPKM 240
181 QFACMEPHRDYDSFVCLVSRGGSQSVYGVQDTHSGPLPHHRRMFMGDSFCPLAGKPKM 240

QY 241 PFQNVVSDGQLEDSSLLLEVDGPAKKNVEFKAQKRGCLCTVHREADFFWSLCTADMSLLE 300
DB 241 PFQNVVSDGQLEDSSLLLEVDGPAKKNVEFKAQKRGCLCTVHREADFFWSLCTADMSLLE 300
QY 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITESKDMHFFSLGCLLDVL 348
DB 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITESKDMHFFSLGCLLDVL 348

RESULT 4
US-10-755-889-102
; Sequence 102, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF- κ B
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 102
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-102

Query Match 98.6%; Score 1774; DB 16; Length 462;
Best Local Similarity 94.5%; Pred. No. 5.8e-158;
Matches 346; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKSEKSFLLDLVVELEKLNVLVAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKSEKSFLLDLVVELEKLNVLVAPDQDLLEKCL 156
QY 61 KNHRIIDLTKTKIQYKQSQVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106
DB 157 KNHRIIDLTKTKIQYKQSQVQAGTSYRNVLQAAIQKSLKDPNNFRLLHNGRSKEQRLKEQ 216
QY 107 ----BEPVKKSQSEAFIPQSIPEERYKMKSKPLGICLIIDCIGNETELLRTFTSLGY 162
DB 217 LGAQQEPVKKSQSEAFIPQSIPEERYKMKSKPLGICLIIDCIGNETELLRTFTSLGY 276
QY 163 EVQKFLHLSMHGISOILGQFACMPHEHRDYSFVCLVSRGGSQSVYGVVDQTHSGPLHHI 222
DB 277 EVQKFLHLSMHGISOILGQFACMPHEHRDYSFVCLVSRGGSQSVYGVVDQTHSGPLHHI 336
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DB 337 RMFMGDCSPYLAKPKMFFIQQNYVVSQGLDSSLLLEVDGPAKKNVEFKAQKRGCLCTVH 396
QY 283 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQERTIPGSGITESKDMHFFSLGC 342
DB 397 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQERTIPGSGITESKDMHFFSLGC 456
QY 343 ILLDVL 348
DB 457 ILLDVL 462

RESULT 5
US-09-861-270-2
; Sequence 2, Application US/09861270
; Patent No. US20020052474A1
; GENERAL INFORMATION:
; APPLICANT: Sul, Hong-Bing
; Goeddel, David V.

; TITLE OF INVENTION: Regulators of Apoptosis
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESS: Science & Technology Law Group
; STREET: 75 Denise Drive
; CITY: Hillsborough
; STATE: California
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/861,270
; FILING DATE: 18-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,088
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ogman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-861-270-2

Query Match 90.8%; Score 1635; DB 9; Length 480;
Best Local Similarity 94.1%; Pred. No. 7.5e-145;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKSEKSFLLDLVVELEKLNVLVAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKSEKSFLLDLVVELEKLNVLVAPDQDLLEKCL 156
QY 61 KNHRIIDLTKTKIQYKQSQVQAGTSYRNVLQAAIQKSLKDPNNFR----- 106
DB 157 KNHRIIDLTKTKIQYKQSQVQAGTSYRNVLQAAIQKSLKDPNNFRLLHNGRSKEQRLKEQ 216
QY 107 ----BEPVKKSQSEAFIPQSIPEERYKMKSKPLGICLIIDCIGNETELLRTFTSLGY 162
DB 217 LGAQQEPVKKSQSEAFIPQSIPEERYKMKSKPLGICLIIDCIGNETELLRTFTSLGY 276
QY 163 EVQKFLHLSMHGISOILGQFACMPHEHRDYSFVCLVSRGGSQSVYGVVDQTHSGPLHHI 222
DB 277 EVQKFLHLSMHGISOILGQFACMPHEHRDYSFVCLVSRGGSQSVYGVVDQTHSGPLHHI 336
QY 223 RMFMGDCSPYLAKPKMFFIQQNYVVSQGLDSSLLLEVDGPAKKNVEFKAQKRGCLCTVH 282
DB 337 RMFMGDCSPYLAKPKMFFIQQNYVVSQGLDSSLLLEVDGPAKKNVEFKAQKRGCLCTVH 396
QY 283 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
DB 397 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 435

RESULT 6
US-09-410-194-11
; Sequence 11, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg

```
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmier, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-11

Query Match          90.8%; Score 1635; DB 9; Length 480;
Best Local Similarity 94.1%; Pred. No. 7.5e-145;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKESFLDLVVELEKLNVLVAPDQDLDLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKESFLDLVVELEKLNVLVAPDQDLDLEKCL 156
QY 61 KNIHRIDLTKTKYKQSVQAGTGYRNVLQAAIQKSLKDPNNPR----- 106
DB 157 KNIHRIDLTKTKYKQSVQAGTGYRNVLQAAIQKSLKDPNNPRFLHNGRSKEQRLKEQ 216
QY 107 ----EPPVKKSTQSEAFIPQSIPEERYKMKSKPGICLIIDICINETELLRDITSLGY 162
DB 217 LGAQQEPVKKSTQSEAFIPQSIPEERYKMKSKPGICLIIDICINETELLRDITSLGY 276
QY 163 EVQKFLHLSMHGSIQILGQFACMPHRRDYDSFVCLVSRGSGSQSVYGVVDQTHSGPLPHHI 222
DB 277 EVQKFLHLSMHGSIQILGQFACMPHRRDYDSFVCLVSRGSGSQSVYGVVDQTHSGPLPHHI 336
QY 223 RRMFMGDCPYLAGPKPMFFIQNYVVSQGLDSSLLLEVDPGAMKNVBFKAQKRGGLCTVH 282
DB 337 RRMFMGDCPYLAGPKPMFFIQNYVVSQGLDSSLLLEVDPGAMKNVBFKAQKRGGLCTVH 396
QY 283 READFFWSLCTADMSLLEQSHSSPSLIYLOCLSQKLRQER 321
DB 397 READFFWSLCTADMSLLEQSHSSPSLIYLOCLSQKLRQER 435

RESULT 7
US-09-410-194-17
; Sequence 17, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmier, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
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```
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-17

Query Match          90.8%; Score 1635; DB 9; Length 480;
Best Local Similarity 94.1%; Pred. No. 7.5e-145;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKESFLDLVVELEKLNVLVAPDQDLDLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGGRGKISKESFLDLVVELEKLNVLVAPDQDLDLEKCL 156
QY 61 KNIHRIDLTKTKYKQSVQAGTGYRNVLQAAIQKSLKDPNNPR----- 106
DB 157 KNIHRIDLTKTKYKQSVQAGTGYRNVLQAAIQKSLKDPNNPRFLHNGRSKEQRLKEQ 216
QY 107 ----EPPVKKSTQSEAFIPQSIPEERYKMKSKPGICLIIDICINETELLRDITSLGY 162
DB 217 LGAQQEPVKKSTQSEAFIPQSIPEERYKMKSKPGICLIIDICINETELLRDITSLGY 276
QY 163 EVQKFLHLSMHGSIQILGQFACMPHRRDYDSFVCLVSRGSGSQSVYGVVDQTHSGPLPHHI 222
DB 277 EVQKFLHLSMHGSIQILGQFACMPHRRDYDSFVCLVSRGSGSQSVYGVVDQTHSGPLPHHI 336
QY 223 RRMFMGDCPYLAGPKPMFFIQNYVVSQGLDSSLLLEVDPGAMKNVBFKAQKRGGLCTVH 282
DB 337 RRMFMGDCPYLAGPKPMFFIQNYVVSQGLDSSLLLEVDPGAMKNVBFKAQKRGGLCTVH 396
QY 283 READFFWSLCTADMSLLEQSHSSPSLIYLOCLSQKLRQER 321
DB 397 READFFWSLCTADMSLLEQSHSSPSLIYLOCLSQKLRQER 435

RESULT 8
US-09-009-893-2
; Sequence 2, Application US/09009893
; Publication No. US20030087339A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: GENTZ, REINER L.
; APPLICANT: KENNY, JOSEPH J.
; TITLE OF INVENTION: I-FICE, A NOVEL INHIBITOR OF TUMOR
; TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APOPTOSIS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,893
; FILING DATE: HERewith
```

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; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 60/034,205
; FILING DATE: 21-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/054,800
; FILING DATE: 05-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0970002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-009-893-2

Query Match          90.8%; Score 1635; DB 10; Length 480;
Best Local Similarity 94.1%; Pred. No. 7.5e-145;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDLVVELEKLNLVAPDQDLDLEKCL 60
Db 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDLVVELEKLNLVAPDQDLDLEKCL 156
QY 61 KNIHRIDLTKIQYKQSVQAGTSYRNVLAQAIQKSLKDPNNR----- 106
Db 157 KNIHRIDLTKIQYKQSVQAGTSYRNVLAQAIQKSLKDPNNRFLNNGRSKEQRLKEQ 216
QY 107 ----EPPVKYSIQSEAFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDFTTSLGY 162
Db 217 LQAQEPVKYSIQSEAFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDFTTSLGY 276
QY 163 EVQKFLHLSMHGISQILGQFACMPHRYDYSFVCLVSRGSGSVYGVVDQTHSGPLPHHI 222
Db 277 EVQKFLHLSMHGISQILGQFACMPHRYDYSFVCLVSRGSGSVYGVVDQTHSGPLPHHI 336
QY 223 RMFMGDCPCYLAGPKMFFIQNYVVSQGLDSSLLLEVDGPMKNVFEKAKRGGLCTVH 282
Db 337 RMFMGDCPCYLAGPKMFFIQNYVVSQGLDSSLLLEVDGPMKNVFEKAKRGGLCTVH 396
QY 283 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
Db 397 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 435

RESULT 9
US-09-471-749-1
; Sequence 1, Application US/09471749
; Publication No. US20030124113A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Patterson, Chandra
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN APOPTOSIS ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
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; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/471,749
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/078,402
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PP-0519 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: TBP1LB02
; CLONE: 157658
US-09-471-749-1

Query Match          90.8%; Score 1635; DB 10; Length 480;
Best Local Similarity 94.1%; Pred. No. 7.5e-145;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDLVVELEKLNLVAPDQDLDLEKCL 60
Db 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDLVVELEKLNLVAPDQDLDLEKCL 156
QY 61 KNIHRIDLTKIQYKQSVQAGTSYRNVLAQAIQKSLKDPNNR----- 106
Db 157 KNIHRIDLTKIQYKQSVQAGTSYRNVLAQAIQKSLKDPNNRFLNNGRSKEQRLKEQ 216
QY 107 ----EPPVKYSIQSEAFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDFTTSLGY 162
Db 217 LQAQEPVKYSIQSEAFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDFTTSLGY 276
QY 163 EVQKFLHLSMHGISQILGQFACMPHRYDYSFVCLVSRGSGSVYGVVDQTHSGPLPHHI 222
Db 277 EVQKFLHLSMHGISQILGQFACMPHRYDYSFVCLVSRGSGSVYGVVDQTHSGPLPHHI 336
QY 223 RMFMGDCPCYLAGPKMFFIQNYVVSQGLDSSLLLEVDGPMKNVFEKAKRGGLCTVH 282
Db 337 RMFMGDCPCYLAGPKMFFIQNYVVSQGLDSSLLLEVDGPMKNVFEKAKRGGLCTVH 396
QY 283 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 321
Db 397 READFFWSLCTADMSLLEQSHSSPSLYLQCLSQKLRQER 435

RESULT 10
US-10-713-208-2
; Sequence 2, Application US/10713208
; Publication No. US20040121387A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: I-FLICE, A Novel Inhibitor of Tumor Necrosis Factor Receptor-1 and
; FILE OF INVENTION: CD-95 Induced Apoptosis
; FILE REFERENCE: PF381C1D1
; CURRENT APPLICATION NUMBER: US/10/713,208
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: US 09/489,155
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/009,893
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: US 60/054,800
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/034,205
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; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-713-208-2

Query Match          90.8%; Score 1635; DB 16; Length 480;
Best Local Similarity 94.1%; Pred. No. 7.5e-145;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKEKSFDLVVELEKLNLVAPDQDLDLEKCL 60
Db 97 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKEKSFDLVVELEKLNLVAPDQDLDLEKCL 156
QY 61 KNIHRIDLTKTIQKYKQSVQAGTSYRNVLAQAIOKSLKDPNNFR----- 106
Db 157 KNIHRIDLTKTIQKYKQSVQAGTSYRNVLAQAIOKSLKDPNNFRNLHNGRSKEQRLKEQ 216
QY 107 ----EPPVKYSIQSEAFLPQSIPEERYKMKSPKIGICLIIDCIGNETELLRTDFTSLGY 162
Db 217 LGAQOEPVKYSIQSEAFLPQSIPEERYKMKSPKIGICLIIDCIGNETELLRTDFTSLGY 276
QY 163 EVQKFLHLSMHGISOILGQFACMPHRDYSFVCVLVSRGGSQSVYGVDTHTSGGLPLHHI 222
Db 277 EVQKFLHLSMHGISOILGQFACMPHRDYSFVCVLVSRGGSQSVYGVDTHTSGGLPLHHI 336
QY 223 RRMFMGDCPYLAGPKMFFIQQYVSDGQLEDSSLLVEDGPMKNVFEKAKRGLCTVH 282
Db 337 RRMFMGDCPYLAGPKMFFIQQYVSDGQLEDSSLLVEDGPMKNVFEKAKRGLCTVH 396
QY 283 READFFWSLCTADMSLLSQSHSSPSLYLQCLSQKLRQER 321
Db 397 READFFWSLCTADMSLLSQSHSSPSLYLQCLSQKLRQER 435

RESULT 12
US-10-832-218-17
; Sequence 17, Application US/10832218
; Publication No. US20050084876A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmeler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/10/832,218
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US/09/410,194
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-832-218-17

Query Match          90.8%; Score 1635; DB 17; Length 480;
Best Local Similarity 94.1%; Pred. No. 7.5e-145;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKEKSFDLVVELEKLNLVAPDQDLDLEKCL 60
Db 97 MAEIGEDLDKSDVSSLIPLMKDYMGRGKISKEKSFDLVVELEKLNLVAPDQDLDLEKCL 156
QY 61 KNIHRIDLTKTIQKYKQSVQAGTSYRNVLAQAIOKSLKDPNNFR----- 106
Db 157 KNIHRIDLTKTIQKYKQSVQAGTSYRNVLAQAIOKSLKDPNNFRNLHNGRSKEQRLKEQ 216
QY 107 ----EPPVKYSIQSEAFLPQSIPEERYKMKSPKIGICLIIDCIGNETELLRTDFTSLGY 162
Db 217 LGAQOEPVKYSIQSEAFLPQSIPEERYKMKSPKIGICLIIDCIGNETELLRTDFTSLGY 276
QY 163 EVQKFLHLSMHGISOILGQFACMPHRDYSFVCVLVSRGGSQSVYGVDTHTSGGLPLHHI 222
Db 277 EVQKFLHLSMHGISOILGQFACMPHRDYSFVCVLVSRGGSQSVYGVDTHTSGGLPLHHI 336
QY 223 RRMFMGDCPYLAGPKMFFIQQYVSDGQLEDSSLLVEDGPMKNVFEKAKRGLCTVH 282
Db 337 RRMFMGDCPYLAGPKMFFIQQYVSDGQLEDSSLLVEDGPMKNVFEKAKRGLCTVH 396
QY 283 READFFWSLCTADMSLLSQSHSSPSLYLQCLSQKLRQER 321
Db 397 READFFWSLCTADMSLLSQSHSSPSLYLQCLSQKLRQER 435

RESULT 11
US-10-832-218-11
; Sequence 11, Application US/10832218
; Publication No. US20050084876A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmeler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/10/832,218
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US/09/410,194
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-832-218-11
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Db 157 KNIHRIDLTKIKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFRLHNGRSKEQRLKEQ 216
QY 107 ----EPVKKSIQSEAFIPQSIPEERYKMKSPGLGICLIIDICIGNETELLRTDTFTSLGY 162
Db 217 LGAQOEPVKKSIQSEAFIPQSIPEERYKMKSPGLGICLIIDICIGNETELLRTDTFTSLGY 276
QY 163 EVQKFLHLSMHGISOILGQFACMPHRDYDSFVCVLVSRGGSQSVYGVDTHTSGLPLHHI 222
Db 277 EVQKFLHLSMHGISOILGQFACMPHRDYDSFVCVLVSRGGSQSVYGVDTHTSGLPLHHI 336
QY 223 RRMFMGDSCPYLAGKPKMFPIQNYVVSQGLEDSLSLLEVDGPKMKVFEKAKRGLCTVH 282
Db 337 RRMFMGDSCPYLAGKPKMFPIQNYVVSQGLEDSLSLLEVDGPKMKVFEKAKRGLCTVH 396
QY 283 READPFWSLCTADMSLLEQSHSSPSLYLQCLSKLRQER 321
Db 397 READPFWSLCTADMSLLEQSHSSPSLYLQCLSKLRQER 435

RESULT 13

US-09-764-861-37
; Sequence 37, Application US/09764861
; Publication No. US20020086811A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT204
; CURRENT APPLICATION NUMBER: US/09/764,861
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; FEATURE:
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-861-37

Query Match 90.6%; Score 1630; DB 9; Length 391;
Best Local Similarity 93.8%; Pred. No. 1.6e-144;
Matches 318; Conservative 2; Mismatches 1; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESKSFLLDLVVELEKLNVLAPDQDLLEKCL 60
Db 8 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESKSFLLDLVVELEKLNVLAPDQDLLEKCL 67
QY 61 KNIHRIDLTKIKYKQSVQAGTSYRNVLQAAIQKSLKDPNNF----- 106
Db 68 KNIHRIDLTKIKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFRLHNGRSKEQRLKEQ 127
QY 107 ----EPVKKSIQSEAFIPQSIPEERYKMKSPGLGICLIIDICIGNETELLRTDTFTSLGY 162
Db 128 LGAQOEPVKKSIQSEAFIPQSIPEERYKMKSPGLGICLIIDICIGNETELLRTDTFTSLGY 187
QY 163 EVQKFLHLSMHGISOILGQFACMPHRDYDSFVCVLVSRGGSQSVYGVDTHTSGLPLHHI 222
Db 188 EVQKFLHLSMHGISOILGQFACMPHRDYDSFVCVLVSRGGSQSVYGVDTHTSGLPLHHI 247
QY 223 RRMFMGDSCPYLAGKPKMFPIQNYVVSQGLEDSLSLLEVDGPKMKVFEKAKRGLCTVH 282
Db 248 RRMFMGDSCPYLAGKPKMFPIQNYVVSQGLEDSLSLLEVDGPKMKVFEKAKRGLCTVH 307
QY 283 READPFWSLCTADMSLLEQSHSSPSLYLQCLSKLRQER 321
Db 308 READPFWSLCTADMSLLEQSHSSPSLYLQCLSKLRQER 346

RESULT 14

US-10-103-313-318
; Sequence 318, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ207C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 318
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-103-313-318

US-09-764-861-37
; Sequence 37, Application US/09764861
; Publication No. US20030171252A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT204
; CURRENT APPLICATION NUMBER: US/09/764,861
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-861-37

Query Match 90.6%; Score 1630; DB 10; Length 391;
Best Local Similarity 93.8%; Pred. No. 1.6e-144;
Matches 318; Conservative 2; Mismatches 1; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESKSFLLDLVVELEKLNVLAPDQDLLEKCL 60
Db 8 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESKSFLLDLVVELEKLNVLAPDQDLLEKCL 67
QY 61 KNIHRIDLTKIKYKQSVQAGTSYRNVLQAAIQKSLKDPNNF----- 106
Db 68 KNIHRIDLTKIKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFRLHNGRSKEQRLKEQ 127
QY 107 ----EPVKKSIQSEAFIPQSIPEERYKMKSPGLGICLIIDICIGNETELLRTDTFTSLGY 162
Db 128 LGAQOEPVKKSIQSEAFIPQSIPEERYKMKSPGLGICLIIDICIGNETELLRTDTFTSLGY 187
QY 163 EVQKFLHLSMHGISOILGQFACMPHRDYDSFVCVLVSRGGSQSVYGVDTHTSGLPLHHI 222
Db 188 EVQKFLHLSMHGISOILGQFACMPHRDYDSFVCVLVSRGGSQSVYGVDTHTSGLPLHHI 247
QY 223 RRMFMGDSCPYLAGKPKMFPIQNYVVSQGLEDSLSLLEVDGPKMKVFEKAKRGLCTVH 282
Db 248 RRMFMGDSCPYLAGKPKMFPIQNYVVSQGLEDSLSLLEVDGPKMKVFEKAKRGLCTVH 307
QY 283 READPFWSLCTADMSLLEQSHSSPSLYLQCLSKLRQER 321
Db 308 READPFWSLCTADMSLLEQSHSSPSLYLQCLSKLRQER 346

RESULT 15

US-10-103-313-318
; Sequence 318, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ207C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 318
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-103-313-318

```
Query Match      90.6%; Score 1630; DB 14; Length 391;
Best Local Similarity 93.8%; Pred. No. 1.6e-144;
Matches 318; Conservative 2; Mismatches 1; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKGIKSKSFLDLVVELEKLNLVAPDQDLLEKCL 60
Db 8 MAEIGEDLDKSDVSSLIIFLMKDYMGKGIKSKSFLDLVVELEKLNLVAPDQDLLEKCL 67
QY 61 KNHRIIDLTKIQKYKQSVQGAGTSYRNVLQAAIQKSLADPSNNPR----- 106
Db 68 KNHRIIDLTKIQKYKQSVQGAGTSYRNVLQAAIQKSLADPSNNPRFLHNGRSKEORLKEQ 127
QY 107 ----EEPVKKSIQSEAFIPQSIPEERYKMKSKPLGICLIIDCIGNETELLRTFTSLGY 162
Db 128 LGAQQEPVKKSIQSEAFIPQSIPEERYKMKSKPLGICLIIDCIGNETELLRTFTSLGY 187
QY 163 EVOKFLHLSMHGISQILGQFACWPEHRDYDSFVCLVSRGGSQSVYGVVDQTHSGLPPLHHI 222
Db 188 EVOKFLHLSMHGISQILGQFACWPEHRDYDSFVCLVSRGGSQSVYGVVDQTHSGLPPLHHI 247
QY 223 RRMFMGDCPYLAGKPKMFFIQNYVVSQGLSDSSILEVDGPAMKNVEPKAKRGGLCTVH 282
Db 248 RRMFMGDCPYLAGKPKMFFIQNYVVSQGLSDSSILEVDGPAMKNVEPKAKRGGLCTVH 307
QY 283 READFFWSLCTADMSLLEQSHSSPSLIYLQCLSQKLQER 321
Db 308 READFFWSLCTADMSLLEQSHSSPSLIYLQCLSQKLQER 346
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Search completed: June 20, 2005, 13:17:59
Job time : 164 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1800	100.0	0	348	4	US-09-009-893A-6	Sequence 6, Appli
2	1800	100.0	0	348	4	US-09-489-155-6	Sequence 6, Appli
3	1635	90.18	480	4	US-08-795-088A-2	Sequence 2, Appli	Sequence 2, Appli
4	1635	90.18	480	4	US-09-009-893A-2	Sequence 2, Appli	Sequence 2, Appli
5	1635	90.18	480	4	US-09-489-155-2	Sequence 2, Appli	Sequence 2, Appli
6	1579	87.7	480	3	US-09-069-023-34	Sequence 34, Appli	Sequence 34, Appli
7	1554.5	86.4	445	3	US-08-859-167-2	Sequence 2, Appli	Sequence 2, Appli
8	1554.5	86.4	445	3	US-09-109-273-2	Sequence 2, Appli	Sequence 2, Appli
9	1554.5	86.4	445	3	US-09-276-993-2	Sequence 2, Appli	Sequence 2, Appli
10	1554.5	86.4	445	4	US-09-723-450-2	Sequence 2, Appli	Sequence 2, Appli
11	1270	70.16	244	4	US-09-949-016-11405	Sequence 11405, A	Sequence 11405, A
12	527	29.3	221	3	US-09-382-155-17	Sequence 17, Appli	Sequence 17, Appli
13	527	29.3	221	3	US-09-074-044A-17	Sequence 17, Appli	Sequence 17, Appli
14	383	21.3	84	3	US-09-074-044A-2	Sequence 2, Appli	Sequence 2, Appli
15	369	20.5	84	3	US-09-382-155-2	Sequence 2, Appli	Sequence 2, Appli
16	313	17.4	479	3	US-08-983-502-7	Sequence 7, Appli	Sequence 7, Appli
17	313	17.4	479	4	US-09-516-747-7	Sequence 7, Appli	Sequence 7, Appli
18	313	17.4	479	4	US-09-851-873-101	Sequence 101, App	Sequence 101, App
19	313	17.4	479	5	PCT-US96-10521-7	Sequence 7, Appli	Sequence 7, Appli
20	311.5	17.3	478	4	US-09-009-893A-3	Sequence 3, Appli	Sequence 3, Appli
21	311.5	17.3	478	4	US-09-489-155-3	Sequence 3, Appli	Sequence 3, Appli
22	311	17.3	479	2	US-08-807-200-12	Sequence 12, Appli	Sequence 12, Appli
23	311	17.3	479	3	US-09-382-155-28	Sequence 28, Appli	Sequence 28, Appli
24	311	17.3	479	3	US-09-001-777-12	Sequence 12, Appli	Sequence 12, Appli
25	311	17.3	479	3	US-09-074-044A-26	Sequence 26, Appli	Sequence 26, Appli
26	311	17.3	479	3	US-09-074-044A-27	Sequence 27, Appli	Sequence 27, Appli
27	311	17.3	479	3	US-09-074-044A-28	Sequence 28, Appli	Sequence 28, Appli

QY 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITGSKDMHFSSLGICILLDVL 348
Db 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITGSKDMHFSSLGICILLDVL 348

RESULT 2
US-09-489-155-6
; Sequence 6, Application US/09489155
; Patent No. 6680171
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dixit, Vishva M.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: I-FLICE, A No. 6680171el Inhibitor of Tumor Necrosis Factor Recept
; FILE REFERENCE: 1488.0970002
; CURRENT APPLICATION NUMBER: US/09/489,155
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/009,893
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-155-6

Query Match 100.0%; Score 1800; DB 4; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.7e-183; Indels 0; Gaps 0;
Matches 348; Conservative 0; Mismatches 0;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLDLVVELEKLNLVAPDQDLLEKCL 60
Db 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLDLVVELEKLNLVAPDQDLLEKCL 60

QY 61 KNIHRIDLTKTKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFRLHNGRSKEQRLKEQ 120
Db 61 KNIHRIDLTKTKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFRLHNGRSKEQRLKEQ 120

QY 121 LPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDFTSLGYEVQKFLHLSMHGISQILG 180
Db 121 LPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDFTSLGYEVQKFLHLSMHGISQILG 180

QY 181 QFACMPEHRDYSFVCLVSRGSSQSVYGVDDQTHSGPLPHHRRMPMGDSCPYLAGKPKM 240
Db 181 QFACMPEHRDYSFVCLVSRGSSQSVYGVDDQTHSGPLPHHRRMPMGDSCPYLAGKPKM 240

QY 241 FFIQNVVSDGQLEDSSLELVDPGPMKNVEFPAQKRGCLCTVHREADFFWLSLCTADMSSLE 300
Db 241 FFIQNVVSDGQLEDSSLELVDPGPMKNVEFPAQKRGCLCTVHREADFFWLSLCTADMSSLE 300

QY 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITGSKDMHFSSLGICILLDVL 348
Db 301 QSHSSPSLYLQCLSQKLRQERTIPGSGITGSKDMHFSSLGICILLDVL 348

STREET: 75 Denise Drive
CITY: Hillsborough
STATE: California
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,088A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-795-088A-2

Query Match 90.8%; Score 1635; DB 3; Length 480;
Best Local Similarity 94.1%; Pred. No. 1.2e-165;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLDLVVELEKLNLVAPDQDLLEKCL 60
Db 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLDLVVELEKLNLVAPDQDLLEKCL 156

QY 61 KNIHRIDLTKTKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFRLHNGRSKEQRLKEQ 106
Db 157 KNIHRIDLTKTKYKQSVQAGTSYRNVLQAAIQKSLKDPNNFRLHNGRSKEQRLKEQ 216

QY 107 ---BEPVKKSIQSEAFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDFTTSLGY 162
Db 217 LGAQOQEPVKKSIQSEAFLPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDFTTSLGY 276

QY 163 EVQKFLHLSMHGISQILGQFACMPEHRDYSFVCLVSRGSSQSVYGVDDQTHSGPLPHHI 222
Db 277 EVQKFLHLSMHGISQILGQFACMPEHRDYSFVCLVSRGSSQSVYGVDDQTHSGPLPHHI 336

QY 223 RRMFMGDSCPYLAGKPKMFFIQNVVSDGQLEDSSLELVDPGPMKNVEFPAQKRGCLCTVH 282
Db 337 RRMFMGDSCPYLAGKPKMFFIQNVVSDGQLEDSSLELVDPGPMKNVEFPAQKRGCLCTVH 396

QY 283 READFFWLSLCTADMSSLELVDPGPMKNVEFPAQKRGCLCTVHREADFFWLSLCTADMSSLE 321
Db 397 READFFWLSLCTADMSSLELVDPGPMKNVEFPAQKRGCLCTVHREADFFWLSLCTADMSSLE 435

RESULT 4
US-09-009-893A-2
; Sequence 2, Application US/09009893A
; Patent No. 6623938
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dixit, Vishva M.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Recept
; FILE REFERENCE: 1488.0970002
; CURRENT APPLICATION NUMBER: US/09/009,893A

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; CURRENT FILING DATE: 1998-02-21
; PRIOR APPLICATION NUMBER: US 60/054,800
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-009-893A-2

Query Match
Best Local Similarity 90.8%; Score 1635; DB 4; Length 480;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESFLDLVVELEKLNVLAPDQDLDLEKCL 60
DB MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESFLDLVVELEKLNVLAPDQDLDLEKCL 156

QY 61 KNIHRIDLTKTKIQYKQSVQAGAGTSYRNVLQAAIQKSLKDPNSNFR----- 106
DB KNIHRIDLTKTKIQYKQSVQAGAGTSYRNVLQAAIQKSLKDPNSNFR----- 216

QY 107 ----BEPVKKSTQSEAFIPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDTFTSLGY 162
DB :
217 LGAQQEPVKKSTQSEAFIPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDTFTSLGY 276

QY 163 EVQKFLHLSMHGISQILGQFACMPBHRDYDSFVCLVSRGSGSVYGVVDQTHSGLPLHHI 222
DB EVQKFLHLSMHGISQILGQFACMPBHRDYDSFVCLVSRGSGSVYGVVDQTHSGLPLHHI 336

QY 223 RRMFMGDCPCYLAGKPKMFFIQNYVVSQGLDSSLSLEVDGPMKNVFEKAKRGKGLCTVH 282
DB 337 RRMFMGDCPCYLAGKPKMFFIQNYVVSQGLDSSLSLEVDGPMKNVFEKAKRGKGLCTVH 396

QY 283 READPFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 321
DB 397 READPFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 435

RESULT 6
US-09-069-023-34
; Sequence 34, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-34

Query Match
Best Local Similarity 87.7%; Score 1579; DB 3; Length 480;
Matches 309; Conservative 4; Mismatches 8; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESFLDLVVELEKLNVLAPDQDLDLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESFLDLVVELEKLNVLAPDQDLDLEKCL 156

QY 61 KNIHRIDLTKTKIQYKQSVQAGAGTSYRNVLQAAIQKSLKDPNSNFR----- 106
DB 157 KNIHRIDLTKTKIQYKQSVQAGAGTSYRNVLQAAIQKSLKDPNSNFR----- 216

QY 107 ----BEPVKKSTQSEAFIPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDTFTSLGY 162
DB 217 LGAQQEPVKKSTQSEAFIPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDTFTSLGY 276

QY 163 EVQKFLHLSMHGISQILGQFACMPBHRDYDSFVCLVSRGSGSVYGVVDQTHSGLPLHHI 222
DB 277 EVQKFLHLSMHGISQILGQFACMPBHRDYDSFVCLVSRGSGSVYGVVDQTHSGLPLHHI 336

QY 223 RRMFMGDCPCYLAGKPKMFFIQNYVVSQGLDSSLSLEVDGPMKNVFEKAKRGKGLCTVH 282
DB 337 RRMFMGDCPCYLAGKPKMFFIQNYVVSQGLDSSLSLEVDGPMKNVFEKAKRGKGLCTVH 396

QY 283 READPFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 321
DB 397 READPFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 435

Query Match
Best Local Similarity 94.1%; Score 1635; DB 4; Length 480;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESFLDLVVELEKLNVLAPDQDLDLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKESFLDLVVELEKLNVLAPDQDLDLEKCL 156

QY 61 KNIHRIDLTKTKIQYKQSVQAGAGTSYRNVLQAAIQKSLKDPNSNFR----- 106
DB 157 KNIHRIDLTKTKIQYKQSVQAGAGTSYRNVLQAAIQKSLKDPNSNFR----- 216

QY 107 ----BEPVKKSTQSEAFIPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDTFTSLGY 162
DB :
217 LGAQQEPVKKSTQSEAFIPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDTFTSLGY 276

QY 163 EVQKFLHLSMHGISQILGQFACMPBHRDYDSFVCLVSRGSGSVYGVVDQTHSGLPLHHI 222
DB EVQKFLHLSMHGISQILGQFACMPBHRDYDSFVCLVSRGSGSVYGVVDQTHSGLPLHHI 336

QY 223 RRMFMGDCPCYLAGKPKMFFIQNYVVSQGLDSSLSLEVDGPMKNVFEKAKRGKGLCTVH 282
DB 337 RRMFMGDCPCYLAGKPKMFFIQNYVVSQGLDSSLSLEVDGPMKNVFEKAKRGKGLCTVH 396

QY 283 READPFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 321
DB 397 READPFWSLCTADMSLLEQSHSSPSLYLOCLSQKLRQER 435

RESULT 5
US-09-489-155-2
; Sequence 2, Application US/09489155
; Patent No. 6680171
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dixit, Vishva M.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: I-FLICE, A No. 6680171el Inhibitor of Tumor Necrosis Factor Recept
; TITLE OF INVENTION: CD-95 Induced Apoptosis
; FILE REFERENCE: 1488.0970002
; CURRENT APPLICATION NUMBER: US/09/489,155
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/009,893
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-155-2

Query Match
Best Local Similarity 90.8%; Score 1635; DB 4; Length 480;
Matches 319; Conservative 2; Mismatches 0; Indels 18; Gaps 1;
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```
RESULT 7
US-08-859-167-2
; Sequence 2, Application US/08859167
; Patent No. 6037461
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461iris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,167
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,167
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-859-167-2

Query Match      86.4%; Score 1554.5; DB 3; Length 445;
Best Local Similarity 94.4%; Pred. No. 4.2e-157;
Matches 303; Conservative 1; Mismatches 0; Indels 17; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVVELEKLNLVAPDQLDLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVVELEKLNLVAPDQLDLEKCL 156
QY 61 KNHRIIDLTKIQKYQSQVGAGTSYRNVLQAAIOKSLKDPSPNFPPEPVKSIQSEAF 120
DB 157 KNHRIIDLTKIQKYQSQVGAGTSYRNVLQAAIOKSLKDPSPNFR-----202
QY 121 LPQSIPERYKMKSKPLGICLIIDICIGNETELLRDTFTSLGYEVQKFLHLSMHGISQILG 180
DB 203 ----SIPERYKMKSKPLGICLIIDICIGNETELLRDTFTSLGYEVQKFLHLSMHGISQILG 259
QY 181 QFACMPHERDYDSFVCLVSRGGSQSVYGVQDTHSGPLPLHHIRRMFMGSDCPYLACKPKM 240
DB 260 QFACMPHERDYDSFVCLVSRGGSQSVYGVQDTHSGPLPLHHIRRMFMGSDCPYLACKPKM 319
QY 241 FFIQNTVYSDGQLEDSSLLLEVDPGAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSSLE 300
DB 320 FFIQNTVYSDGQLEDSSLLLEVDPGAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSSLE 379
QY 301 QSHSSPSLYLQCLISOKLROER 321
DB 380 QSHSSPSLYLQCLISOKLROER 400

RESULT 8
US-09-109-273-2
; Sequence 2, Application US/09109273
; Patent No. 6063760
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760iris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/109,273
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,167
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-109-273-2

Query Match      86.4%; Score 1554.5; DB 3; Length 445;
Best Local Similarity 94.4%; Pred. No. 4.2e-157;
Matches 303; Conservative 1; Mismatches 0; Indels 17; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVVELEKLNLVAPDQLDLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVVELEKLNLVAPDQLDLEKCL 156
QY 61 KNHRIIDLTKIQKYQSQVGAGTSYRNVLQAAIOKSLKDPSPNFPPEPVKSIQSEAF 120
DB 157 KNHRIIDLTKIQKYQSQVGAGTSYRNVLQAAIOKSLKDPSPNFR-----202
QY 121 LPQSIPERYKMKSKPLGICLIIDICIGNETELLRDTFTSLGYEVQKFLHLSMHGISQILG 180
DB 203 ----SIPERYKMKSKPLGICLIIDICIGNETELLRDTFTSLGYEVQKFLHLSMHGISQILG 259
QY 181 QFACMPHERDYDSFVCLVSRGGSQSVYGVQDTHSGPLPLHHIRRMFMGSDCPYLACKPKM 240
DB 260 QFACMPHERDYDSFVCLVSRGGSQSVYGVQDTHSGPLPLHHIRRMFMGSDCPYLACKPKM 319
QY 241 FFIQNTVYSDGQLEDSSLLLEVDPGAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSSLE 300
DB 320 FFIQNTVYSDGQLEDSSLLLEVDPGAMKNVEFKAQKRGCLCTVHREADFFWSLCTADMSSLE 379
QY 301 QSHSSPSLYLQCLISOKLROER 321
DB 380 QSHSSPSLYLQCLISOKLROER 400
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RESULT 9
US-09-276-993-2
; Sequence 2, Application US/09276993
; Patent No. 6207801
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emdad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801iris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/276,993
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,167
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-276-993-2

Query Match 86.4%; Score 1554.5; DB 3; Length 445;
Best Local Similarity 94.4%; Pred. No. 4.2e-157;
Matches 303; Conservative 1; Mismatches 0; Indels 17; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVVELEKLNVLAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVVELEKLNVLAPDQDLLEKCL 156

QY 61 KNIHRIDLTKIKYKQSVQAGTSYRNVLQAAIQSLKDPSPNFPREEPVKSIQSEAF 120
DB 157 KNIHRIDLTKIKYKQSVQAGTSYRNVLQAAIQSLKDPSPNFR----- 202

QY 121 LPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDFTSLGYEVQKFLHLSMHGISOILG 180
DB 203 ---SIPEERYKMKSKPLGICLIIDICIGNETELLRTDFTSLGYEVQKFLHLSMHGISOILG 259

QY 181 QFACMPHERDYDSFVCLVSRGSGSVYGVQDTHSGSLPLHHIRRMFPGDSCPYLAGPKM 240
DB 260 QFACMPHERDYDSFVCLVSRGSGSVYGVQDTHSGSLPLHHIRRMFPGDSCPYLAGPKM 319

QY 241 FTQNYVSDGLEDSSLLLEVDPKMNVEFKAQKRGCTVHREADFFWSLCTADMSSLE 300
DB 320 FTQNYVSDGLEDSSLLLEVDPKMNVEFKAQKRGCTVHREADFFWSLCTADMSSLE 379

QY 301 QSHSSPSLYLQCLSQKLRQER 321
DB 380 QSHSSPSLYLQCLSQKLRQER 400

RESULT 11
US-09-949-016-11405
; Sequence 11405, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

RESULT 10
US-09-723-450-2
; Sequence 2, Application US/09723450
; Patent No. 6576751
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emdad S.
; TITLE OF INVENTION: FADD-Like Anti-Apoptotic Molecules, Methods Of Making The Same,
; TITLE OF INVENTION: Compositions For And Methods Of Making The Same
; FILE REFERENCE: TJU2445
; CURRENT APPLICATION NUMBER: US/09/723,450
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/276,993
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/859,167
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. 6576751el Sequence
US-09-723-450-2

Query Match 86.4%; Score 1554.5; DB 4; Length 445;
Best Local Similarity 94.4%; Pred. No. 4.2e-157;
Matches 303; Conservative 1; Mismatches 0; Indels 17; Gaps 1;

QY 1 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVVELEKLNVLAPDQDLLEKCL 60
DB 97 MAEIGEDLDKSDVSSLIIFLMKDYMGKISKEKSFLLDVVELEKLNVLAPDQDLLEKCL 156

QY 61 KNIHRIDLTKIKYKQSVQAGTSYRNVLQAAIQSLKDPSPNFPREEPVKSIQSEAF 120
DB 157 KNIHRIDLTKIKYKQSVQAGTSYRNVLQAAIQSLKDPSPNFR----- 202

QY 121 LPQSIPEERYKMKSKPLGICLIIDICIGNETELLRTDFTSLGYEVQKFLHLSMHGISOILG 180
DB 203 ---SIPEERYKMKSKPLGICLIIDICIGNETELLRTDFTSLGYEVQKFLHLSMHGISOILG 259

QY 181 QFACMPHERDYDSFVCLVSRGSGSVYGVQDTHSGSLPLHHIRRMFPGDSCPYLAGPKM 240
DB 260 QFACMPHERDYDSFVCLVSRGSGSVYGVQDTHSGSLPLHHIRRMFPGDSCPYLAGPKM 319

QY 241 FTQNYVSDGLEDSSLLLEVDPKMNVEFKAQKRGCTVHREADFFWSLCTADMSSLE 300
DB 320 FTQNYVSDGLEDSSLLLEVDPKMNVEFKAQKRGCTVHREADFFWSLCTADMSSLE 379

QY 301 QSHSSPSLYLQCLSQKLRQER 321
DB 380 QSHSSPSLYLQCLSQKLRQER 400

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,044A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLLINS, JOHN M
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 26588
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: not relevant
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-074-044A-2

Query Match 21.3%; Score 383; DB 3; Length 84;
Best Local Similarity 100.0%; Pred. No. 4e-33;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEIGDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNLVAPDQDLDLEKCL 60
Db 8 MAEIGDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNLVAPDQDLDLEKCL 67
QY 61 KNIHRIDLTKTKIQYKQ 77
Db 68 KNIHRIDLTKTKIQYKQ 84

RESULT 15
US-09-382-155-2
Sequence 2, Application US/09382155B
Patent No. 6160095
GENERAL INFORMATION:
APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
FILE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
FILE REFERENCE: Chaudhary
CURRENT APPLICATION NUMBER: US/09/382,155B
CURRENT FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 09/074,044
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 84
TYPE: PRT
ORGANISM: HUMAN HERPESVIRUS 8
US-09-382-155-2

Query Match 20.5%; Score 369; DB 3; Length 84;
Best Local Similarity 97.4%; Pred. No. 1.3e-31;
Matches 75; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MAEIGDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNLVAPDQDLDLEKCL 60
Db 8 MAEIGDLDKSDVSSLIFLMKDYMGRGKISKESFLDLVVELEKLNLVAPDQDLDLEKCL 67
QY 61 KNIHRIDLTKTKIQYKQ 77
Db 68 KNIHRIDLTKTKIQYKQ 84

Search completed: June 20, 2005, 13:06:55
Job time : 44 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 13:07:04 ; Search time 38 Seconds
(without alignments)
189.902 Million cell updates/sec

Title: US-10-713-208-6_COPY_1_75
Perfect score: 373
Sequence: 1 MAEIGEDLDKSDVSSLIPLM.....LEKCLKNIHRIDLTKTIQKY 75

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 23404

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	15.0	60	2 I39957	degradative enzyme
2	53.5	14.3	59	2 C36493	H+-transporting tw
3	53	14.2	48	2 H83759	hypothetical prote
4	50.5	13.5	66	2 AF3493	hypothetical cytos
5	50.5	13.5	68	2 F69799	hypothetical prote
6	49.5	13.3	70	2 B64497	hypothetical prote
7	48.5	13.0	66	2 G71834	ribosomal protein
8	48.5	13.0	66	2 T00821	hypothetical prote
9	47.5	12.7	62	2 T12832	hypothetical prote
10	47	12.6	40	2 S45688	glutathione transf
11	46	12.3	46	2 C81322	very hypothetical
12	45.5	12.2	44	2 F70275	hypothetical prote
13	45.5	12.2	58	2 D89871	conserved hypothet
14	45.5	12.2	60	2 T12910	hypothetical prote
15	45	12.1	45	2 B43959	ORF overlapping ca
16	45	12.1	60	2 A34945	transcription regu
17	45	12.1	62	2 S77797	phosphopyruvate hy
18	45	12.1	62	2 C90761	probable division
19	45	12.1	62	2 H85624	hypothetical prote
20	45	12.1	72	2 B69705	transcription regu
21	45	12.1	74	2 A10546	hypothetical prote
22	45	12.1	74	2 E84127	hypothetical prote
23	44.5	11.9	66	2 G64883	ribosomal protein
24	44.5	11.9	71	2 T07852	probable DNA-direc
25	44	11.8	66	2 T12638	homeotic protein H
26	44	11.8	71	2 AC2362	30S ribosomal prot
27	44	11.8	73	2 T38402	hypothetical prote
28	43.5	11.7	30	2 S34761	L-serine ammonia-1
29	43.5	11.7	64	2 T39013	hypothetical prote

30	43	11.5	70	2 S77883	hypothetical prote
31	42.5	11.4	65	2 C82339	hypothetical prote
32	42.5	11.4	66	2 C97870	oxidoreductase hom
33	42.5	11.4	74	2 E90827	hypothetical prote
34	42.5	11.4	74	2 C96547	hypothetical prote
35	42	11.3	57	2 C97758	hypothetical prote
36	42	11.3	65	2 T03652	probable carbonate
37	42	11.3	70	2 S48885	DNA-directed RNA p
38	41.5	11.1	65	2 C82290	hypothetical prote
39	41.5	11.1	67	2 H96936	probable metal-bin
40	41.5	11.1	72	2 G72399	ribosomal protein
41	41.5	11.1	73	2 E95078	conserved hypothet
42	41.5	11.1	75	2 AB1245	exodeoxyribonuclea
43	41.5	11.1	75	2 AF1607	exodeoxyribonuclea
44	41	11.0	40	2 T07583	hypothetical prote
45	41	11.0	50	2 H81250	hypothetical prote

ALIGNMENTS

RESULT 1

I39957

degradative enzyme production factor degR - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004

C:Accession: I39957; I39958; A69614

R:Nagami, Y.; Tanaka, T.

J. Bacteriol. 166, 20-28, 1986

A:Title: Molecular cloning and nucleotide sequence of a DNA fragment from Bacillus natto

A:Reference number: I39957; MUID:86168015; PMID:3082853

A:Accession: I39957

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-60 <RES>

A:Cross-references: UNIPROT:P06563; GB:M12917; NID:g143354; PIDN:AAA22671.1; PID:g143355

R:Yang, M.; Shimotzu, H.; Ferrari, E.; Henner, D.J.

J. Bacteriol. 169, 434-437, 1987

A:Title: Characterization and mapping of the Bacillus subtilis prtr gene.

A:Reference number: I39958; MUID:87083406; PMID:3098734

A:Accession: I39958

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-60 <RE2>

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertet

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,

Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot,

akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Torato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.

A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:980404033; PMID:9384377

A:Accession: A69614

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-60 <KUN>

A:Cross-references: GB:Z99115; GB:AL009126; NID:g2634478; PIDN:CAB14112.1; PID:e1183641;

C:Genetics:

A:Gene: degR

Query Match 15.0%; Score 56; DB 2; Length 60;

Best Local Similarity 27.8%; Pred. No. 45;

Matches 15; Conservative 14; Mismatches 17; Indels 8; Gaps 1;

QY	28	KISKEKSFLLDVVELEKLNVLAPDQDLLEK-----CLKNIHRIIDUKTRIQ 73
Db	7	KLILHKTFFIEYDLBEELADIAKPKGSMKYEVEIEQRCKQNILAIETQMNIK 60
RESULT 2		
C36493		
H+-transporting two-sector ATPase (EC 3.6.3.14) epsilon chain - Sulfolobus acidocaldarius		
C:Species: Sulfolobus acidocaldarius		
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004		
C:Accession: C36493		
R:Onda, K.; Konishi, J.; Hajiro, K.; Oshima, T.; Date, T.; Yoshida, M.		
J. Biol. Chem. 265, 21509-21513, 1990		
A:Title: Structure of an ATPase operon of an acidothermophilic archaeobacterium, Sulfolob		
A:Reference number: A36493, MUID:91072342; PMID:2147683		
A:Accession: C36493		
A:Status: preliminary		
A:Molecule type: DNA		
A:Residues: 1-59 <DEN>		
A:Cross-references: UNIPROT:P62018; GB:M57238; GB:J05671; NID:g152915; PID:g152918		
C:Keywords: hydrolase		
Query Match 14.3%; Score 53.5; DB 2; Length 59;		
Best Local Similarity 30.6%; Pred. No. 79;		
Matches 22; Conservative 14; Mismatches 17; Indels 19; Gaps 5;		
QY	7	DLDKDVSSLIFLMKDYMGRGKISKEKSFLLDVVELEKLN-----VAPQDLLEKLN 62
Db	3	EDKSTIDKYINILK-----SKLDQKKNEI-----LSKINMEYKTLKORLDELEKLN 52
QY	63	IHRIDLKTKIQK 74
Db	53	I-----LK-EVQK 59
RESULT 3		
Hypothetical protein BH0880 [imported] - Bacillus halodurans (strain C-125)		
C:Species: Bacillus halodurans		
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004		
C:Accession: H83759		
R:Takami, H.; Nakasono, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira		
Nucleic Acids Res. 28, 4317-4331, 2000		
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and		
A:Reference number: A83650, MUID:20512582; PMID:11058132		
A:Accession: H83759		
A:Status: preliminary		
A:Molecule type: DNA		
A:Residues: 1-48 <STO>		
A:Cross-references: UNIPROT:O9KEH2; GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BA045		
A:Experimental source: strain C-125		
C:Genetics:		
A:Gene: BH0880		
Query Match 14.2%; Score 53; DB 2; Length 48;		
Best Local Similarity 41.3%; Pred. No. 71;		
Matches 19; Conservative 6; Mismatches 11; Indels 10; Gaps 2;		
QY	24	MGRGKISKEKSFLLDVVELEKLNVLAPDQDLLEKLNHRIIDLK 69
Db	1	MGR-----KLLSPFELVLENKELLNDPEQLSKIEK-----RLDEK 36
RESULT 4		
AF3493		
Hypothetical cytosolic protein BME11932 [imported] - Brucella melitensis (strain 16M)		
C:Species: Brucella melitensis		
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004		
C:Accession: AF3493		
R:DelVecchio, V.G.; Kapatalal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,		
; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess		
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002		

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis		
A:Reference number: AD3252; PMID:11756688		
A:Accession: AF3493		
A:Status: preliminary		
A:Molecule type: DNA		
A:Residues: 1-66 <KOR>		
A:Cross-references: UNIPROT:Q8YEE6; GB:AE008917; PIDN:AAL53113.1; PID:g17983979; GSPDB:G		
A:Experimental source: strain 16M		
C:Genetics:		
A:Gene: BME11932		
A:Map position: 1		
Query Match 13.5%; Score 50.5; DB 2; Length 66;		
Best Local Similarity 31.2%; Pred. No. 1.8e+02;		
Matches 15; Conservative 9; Mismatches 13; Indels 11; Gaps 2;		
QY	24	MGRGKISKEKSFLLDVVEL-----EKLNV-----APQDLLEKCL 60
Db	1	MQRYRFDKRIITLTAIVELNQGIEPEDLDLVLSRIGPVDLDMQECFL 48
RESULT 5		
F69799		
Hypothetical protein yezA - Bacillus subtilis		
C:Species: Bacillus subtilis		
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004		
C:Accession: F69799		
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter		
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho		
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.		
Nature 390, 249-256, 1997		
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler		
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;		
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,		
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Mauda, S.; Mause		
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,		
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,		
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,		
Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Terpstra, J.; Tosato, V.; Uchiyama,		
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.		
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. Bacillus subtilis.		
A:Title: The complete genome sequence of the Gram-positive bacterium		
A:Reference number: A69580; MUID:98044033; PMID:9384377		
A:Accession: F69799		
A:Status: preliminary; nucleic acid sequence not shown; translation not shown		
A:Molecule type: DNA		
A:Residues: 1-68 <KUN>		
A:Cross-references: UNIPROT:O31505; GB:Z99107; GB:AL009126; NID:g2632866; PIDN:CAB12500.1		
A:Experimental source: strain 168		
C:Genetics:		
A:Gene: yezA		
Query Match 13.5%; Score 50.5; DB 2; Length 68;		
Best Local Similarity 39.2%; Pred. No. 1.9e+02;		
Matches 20; Conservative 7; Mismatches 17; Indels 7; Gaps 4;		
QY	8	LDKSDVSSLIFLMKMGGRGKISKEK--SFLLDVVELEKLNVLAPDQLDLL 56
Db	1	MDKLTKEELIFLVKELM-NPTLDDEKVEYLDL---LEK-NVPYPAPSLI 46
RESULT 6		
B64497		
Hypothetical protein MJ1579 - Methanococcus jannaschii		
C:Species: Methanococcus jannaschii		
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004		
C:Accession: B64497		
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, S		
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;		
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.		
Science 273, 1058-1073, 1996		
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.		
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.		

Nature 402, 761-768, 1999

A>Title: Sequence and analysis of chromosomes 2 of the plant Arabidopsis thaliana.
A|Reference number: A84420; MUID:20083487; PMID:10617197
A|Accession: D84844
A>Status: preliminary
A|Molecule type: DNA
A|Residues: 1-66 <STO>
A|Cross-references: GB:AE002093; NID:g2618700; PIDN:AAB84347.1; GSPDB:GN00139
C|Genetics:
A|Gene: At2g41650; T32G6.17
A|Map position: 2
A|Introns: 5/2

Query Match 13.0%; Score 48.5; DB 2; Length 66;
Best Local Similarity 38.6%; Pred. No. 2.9e+02;
Matches 17; Conservative 9; Mismatches 13; Indels 5; Gaps 2;

DQ 27 GKTSKE---KSFGLDVLVELE-KLNLVAPDOLDLLEKCLKNIIH 65
||| | : ||| : : : ||| |
Db 10 KGSKPENGUKFUEALKAADKTUSKEELELEKLKNVAR 53

RESULT 9

T12832

hypothetical protein yonU - Bacillus subtilis phage SPBc2

C|Species: Bacillus subtilis phage SPBc2
C|Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C|Accession: T12832; D69915
R|Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Maue, C.; Karamata, D.
submitted to the EMBL Data Library, August 1997
A|Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 prophage
A|Reference number: T12583
A|Accession: T12832
A>Status: preliminary; translated from GB/EMBL/DDBJ
A|Molecule type: DNA
A|Residues: 1-62 <LAZ>
A|Cross-references: UNIPROT:O64081; EMBL:AF020713; NID:g3025478; PID:g3025546; PIDN:AAC1
R|Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero,
C.; Bron, S.; Braillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chou
A.; Ehrlich, S.D.; Emmerxon, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.,
Nature 390, 249-256, 1997
A|Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert,
Iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.,
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A|Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue,
Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A|Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A|Authors: Yoshikawa, H.P.; Zumsteiner, E.; Yoshikawa, H.; Danchin, A.
A|Title: The complete genome sequence of the Gran-positive bacterium Bacillus subtilis.
A|Reference number: A69580; MUID:98044033; PMID:9384377
A|Accession: D69915
A>Status: nucleic acid sequence not shown; translation not shown
A|Molecule type: DNA
A|Residues: 1-62 <KUN>
A|Cross-references: GB:D99115; GB:AL009126; NID:g2634478; PIDN:CABI4017.1; PID:eil83546;
A|Experimental source: strain 168
C|Genetics:
A|Gene: yonU

Query Match 12.7%; Score 47.5; DB 2; Length 62;
Best Local Similarity 35.0%; Pred. No. 3.4e+02;
Matches 14; Conservative 8; Mismatches 7; Indels 11; Gaps 2;

DQ 32 EKSFGLDVLVELEKLNLVAPDOLDLLEKCLKNIIH-----RID 67
||| | : ||| : : : ||| |
Db 2 EKFLDAIQLTGK-----ELEMKKIDSISKEATVRID 34

RESULT 10

S45688

glutathione transferase (EC 2.5.1.18), cardiac - human (fragments)
N/Alternate names: glutathione S-transferase
C:Species: Homo sapiens (man)
C>Date: 10-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: S45688
R:Singhal, S.S.; Zimniak, P.; Awasthi, S.; Piper, J.T.; He, N.; Teng, J.I.; Petersen, D.
Arch. Biochem. Biophys. 311, 242-250, 1994
A:Title: Several closely related glutathione S-transferase isozymes catalyzing conjugati
A:Reference number: S45687; MUID:94263197; PMID:8203886
A:Accession: S45688
A:Molecule type: protein
A:Residues: 1-20;21-40 <SIN>
A:Cross-references: UNIPROT:Q9UDH3
C:Superfamily: glutathione transferase
C:Keywords: cardiac muscle; heart; transferase

Query Match 12.6%; Score 47; DB 2; Length 40;
Best Local Similarity 38.7%; Pred. No. 2.4e+02;
Matches 12; Conservative 11; Mismatches 6; Indels 2; Gaps 2;
QY 31 KEKSFDLVVELEKLNLVAPDQDLLEKCLK 61
DB 12 KEESY-DL-IKVEELSLYVNERPLLOAFIK 40

RESULT 11
CB1372
very hypothetical protein Cj0974 [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: CB1372
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: AB1250; MUID:20150912; PMID:10688204
A:Accession: CB1372
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-46 <PAR>
A:Cross-references: UNIPROT:Q9PNW4; GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CB7323
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj0974

Query Match 12.3%; Score 46; DB 2; Length 46;
Best Local Similarity 38.1%; Pred. No. 3.5e+02;
Matches 16; Conservative 7; Mismatches 17; Indels 2; Gaps 2;
QY 28 KISKESFDLVVELE-KLNLVAPDQDLLEKCLKNIHRIDL 68
DB 6 KIQKVSLLDLVKKLNKQSLKIKQTNTKEN-LNKTHYLT 46

RESULT 12
F70225
hypothetical protein BBE11 - Lyme disease spirochete plasmid E/1p25
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: F70225
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: F70225
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-44 <KLE>
A:Cross-references: UNIPROT:O50707; GB:AE000785; NID:g2689951; PIDN:AAC66044.1; PID:g268
A:Experimental source: strain B31

C:Genetics:
A:Genome: plasmid

Query Match 12.2%; Score 45.5; DB 2; Length 44;
Best Local Similarity 27.5%; Pred. No. 3.7e+02;
Matches 11; Conservative 10; Mismatches 12; Indels 7; Gaps 1;
QY 31 KEKSFDLVVELEKLNLVAPDQDLLEKCLKNIHRIDLKT 70
DB 11 KEKDLIGIKIEKQK-----NLNVSRLNKNMHLVSKS 43

RESULT 13
D89871
conserved hypothetical protein SAS027 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D89871
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, R.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: AB9758; MUID:21311952; PMID:11418146
A:Accession: D89871
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-58 <KUR>
A:Cross-references: UNIPROT:Q99V64; GB:BA000018; PID:g13700831; PIDN:BABA2127.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: SAS027

Query Match 12.2%; Score 45.5; DB 2; Length 58;
Best Local Similarity 30.4%; Pred. No. 5e+02; 22; Indels 7; Gaps 3;
Matches 17; Conservative 10; Mismatches 22; Indels 7; Gaps 3;
QY 11 SDVSSLFLMKDYMGCR-GKISKESFDLVVELEKLNLVAPDQDLLEKCLKNIHR 65
DB 4 AEVGNIVFMDGLGRVEKINDNSVIVDLTI-MENFN-----DLDLPEKTVINHKKR 53

RESULT 14
TI2910
hypothetical protein vory - Bacillus subtilis phage SPBc2
C:Species: Bacillus subtilis phage SPBc2
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: TI2910; A69925
R:Iazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Maue, C.; Karamata, D.
submitted to the EMBL Data Library, August 1997
A:Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 prophag
A:Reference number: Z17583
A:Accession: TI2910
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-60 <LAZ>
A:Cross-references: UNIPROT:O64158; EMBL:AF020713; NID:g3025478; PID:g3025624; PIDN:AAAC13
R:Kunet, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillat, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
A.; Enrich, S.D.; Emerson, P.F.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier
iech, J.; Harwood, C.R.; Hensaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue,
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parco, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Saco, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
keuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377

Search completed: June 20, 2005, 13:22:38
Job time : 40 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	59	15	8	72	2	Q9AHY8
2	56	15	0	60	1	DEGR_BACSU
3	54	14	6	73	1	Q6MSS7
4	53	14	3	59	1	MTPE_SULAC
5	53	14	3	59	1	MTPE_SULTO
6	53	14	2	48	2	Q9KEH2
7	53	14	2	64	2	Q8RI61
8	53	14	2	66	2	Q8GD36
9	53	14	2	73	2	Q7RS48
10	52	13	9	51	2	Q86256
11	52	13	9	51	2	O813F1
12	51	13	8	45	2	Q9RSY9
13	51	13	8	67	2	Q63F79
14	50	13	5	65	2	Q6XD88
15	50	13	5	66	2	Q8YEE6
16	50	13	5	68	2	O31505
17	50	13	4	75	2	Q7YW52
18	49	13	3	70	1	YF79_METJA
19	48	13	0	56	2	Q6LDB8
20	48	13	0	66	1	RL29_HELPJ
21	48	13	0	66	2	O22226
22	48	13	0	68	2	Q6FID6
23	48	13	0	75	2	Q814Q7
24	48	12	9	48	2	Q54872
25	48	12	9	52	1	YORH_HAEIN
26	48	12	9	64	2	Q7P5D9
27	47	12	7	50	2	Q99PT2
28	47	12	7	61	2	Q93AT0
29	47	12	7	62	2	O64081
30	47	12	7	69	2	Q91YA3
31	47	12	7	69	2	Q91YA3
32	47	12	7	69	2	Q91YA3
33	47	12	7	69	2	Q91YA3
34	47	12	7	69	2	Q91YA3
35	47	12	7	69	2	Q91YA3
36	47	12	7	69	2	Q91YA3
37	47	12	7	69	2	Q91YA3
38	47	12	7	69	2	Q91YA3
39	47	12	7	69	2	Q91YA3
40	47	12	7	69	2	Q91YA3
41	47	12	7	69	2	Q91YA3
42	47	12	7	69	2	Q91YA3
43	47	12	7	69	2	Q91YA3
44	47	12	7	69	2	Q91YA3
45	47	12	7	69	2	Q91YA3
46	47	12	7	69	2	Q91YA3
47	47	12	7	69	2	Q91YA3
48	47	12	7	69	2	Q91YA3
49	47	12	7	69	2	Q91YA3
50	47	12	7	69	2	Q91YA3
51	47	12	7	69	2	Q91YA3
52	47	12	7	69	2	Q91YA3
53	47	12	7	69	2	Q91YA3
54	47	12	7	69	2	Q91YA3
55	47	12	7	69	2	Q91YA3
56	47	12	7	69	2	Q91YA3
57	47	12	7	69	2	Q91YA3
58	47	12	7	69	2	Q91YA3
59	47	12	7	69	2	Q91YA3
60	47	12	7	69	2	Q91YA3
61	47	12	7	69	2	Q91YA3
62	47	12	7	69	2	Q91YA3
63	47	12	7	69	2	Q91YA3
64	47	12	7	69	2	Q91YA3
65	47	12	7	69	2	Q91YA3
66	47	12	7	69	2	Q91YA3
67	47	12	7	69	2	Q91YA3
68	47	12	7	69	2	Q91YA3
69	47	12	7	69	2	Q91YA3
70	47	12	7	69	2	Q91YA3
71	47	12	7	69	2	Q91YA3
72	47	12	7	69	2	Q91YA3
73	47	12	7	69	2	Q91YA3
74	47	12	7	69	2	Q91YA3
75	47	12	7</			

```
DEGR_BACSU STANDARD; PRT; 60 AA.
AC P06563;
DT 01-JAN-1988 (Rel. 06, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE Regulatory protein degr.
GN Name=degr; Synonyms=prtr; OrderedLocusNames=BSU21940;
OS Bacillus subtilis, and
OC Bacillus subtilis var. natto.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423, 86029;
RN [1]
SEQUENCE FROM N.A.
RP SPECIES=B.subtilis;
RC MEDLINE=87083406; PubMed=3098734;
RX Yang M., Shimotsu H., Ferrari E., Henner D.J.;
RT "Characterization and mapping of the Bacillus subtilis prtr gene.";
RL J. Bacteriol. 169:434-437(1987).
RN [2]
SEQUENCE FROM N.A.
RP SPECIES=B.subtilis; STRAIN=168 / Marburg;
RC SPECIES=B.subtilis;
RX Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
RA Serror P.;
RT "Sequence analysis of the Bacillus subtilis chromosome region between
the serA and kds loci cloned in a yeast artificial chromosome.";
RL Microbiology 142:2005-2016(1996).
RN [3]
SEQUENCE FROM N.A.
RP SPECIES=B.subtilis; STRAIN=168;
RC SPECIES=B.subtilis; PubMed=9384377; DOI=10.1038/36786;
RX Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borrisier L., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golligty E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S.,
RA Kumano M., Kurita K., Lepidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadale Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Serror S.J., Serror P.,
RA Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takenaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vasearotti A., Viari A., Wambutt R., Wedler E., Wedner H.,
RA Weitzenger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yoshikawa H., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
subtilis.";
RL Nature 390:249-256(1997).
RN [4]
SEQUENCE FROM N.A.
RP SPECIES=B.s.natto;
RX MEDLINE=86168015; PubMed=3082853;
RA Nagami Y., Tanaka T.;
RT "Molecular cloning and nucleotide sequence of a DNA fragment from
Bacillus natto that enhances production of extracellular proteases and
RT levanucrase in Bacillus subtilis.";
RL J. Bacteriol. 166:20-28(1986).
```

CC -!- FUNCTION: Leads, in B.subtilis, to enhanced production of
levansucrase, alkaline protease, and neutral protease. In B.natto
it is nonessential for growth or expression of proteases and
levansucrase.

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DR EMBL; M15318; AAA22672.1; -
DR EMBL; L77246; AAA96622.1; -
DR EMBL; Z99115; CAB14112.1; -
DR EMBL; M12917; AAA22671.1; -
DR PIR; I39957; I39957.
KW Subtilisin; BG10699; degra.
KW Complete proteome; Transcription regulation.
SQ SEQUENCE 60 AA; 7109 MW; C7B7F892FF0AB131 CRC64;

Query Match 15.0%; Score 56; DB 1; Length 60;
Best Local Similarity 27.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 14; Mismatches 17; Indels 8; Gaps 1;

Qy 28 KISKSKSFLDLVVELEKLNVLAPDQLDLLEK-----CLKNIHRIIDLKTKIQ 73
Db 7 KUILHKTFTFIYSDLEELADIAKKGKPSMEKYVEIEQRCKONILAIQMKIK 60

RESULT 3
Q6MS57 PRELIMINARY; PRT; 73 AA.
AC Q6MS57;
ID 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Hypothetical protein.
DE Hypothetical protein.
GN OrderedLocusNames=MSC_0692;
OS Mycoplasma mycoides (subsp. mycoides SC).
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=44101;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PG1;
RX PubMed=14762060; DOI=10.1101/gr.1673304;
RA Westberg J., Persson A., Holmberg A., Goessmann A., Lundberg J.,
RA Johansson K.-E., Pettersson B., Uhlen M.;
RT "The genome sequence of Mycoplasma mycoides subsp. mycoides SC type
strain PG1T, the causative agent of contagious bovine pleuropneumonia
(CBPP).";
RT Genome Res. 14:221-227(2004).
RL EMBL; BX842644; CAE77311.1; -
DR GO; GO:0048037; F:cofactor binding; IEA.
DR InterPro; IPR009081; ACP like.
DR InterPro; IPR006163; Phosphatase_bind.
DR InterPro; IPR006162; Phosphatase_S.
DR Pfam; PF00550; PP-binding; 1.
DR PROSITE; PS00075; ACP DOMAIN; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETINE; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 73 AA; 8309 MW; 1C923FBFC5633609 CRC64;

Query Match 14.6%; Score 54.5; DB 2; Length 73;
Best Local Similarity 33.3%; Pred. No. 6.5e+02;
Matches 19; Conservative 10; Mismatches 9; Indels 19; Gaps 4;

Qy 20 MKDYMGKRGKSKSF-----LDLVVEL-EKLN-LVAPDQ-----DLLE 57
Db 11 LKSRGAKGNITKDSF-KSLGLDLSLMDVMVTEKLNIRISDDQLSLRTIDDLK 67

```
RESULT 4
MTPE SULAC STANDARD; PRT; 59 AA.
AC P62018; P23039;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Membrane-associated ATPase epsilon chain (EC 3.6.3.14) (Sul-ATPase
DE epsilon chain).
GN Name=atpE;
OS Sulfolobus acidocaldarius.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2285;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=91072342; PubMed=2147683;
RA Denda K., Konishi J., Hajiro K., Oshima T., Date T., Yoshida M.;
RT "Structure of an ATPase operon of an acidothermophilic
RT archaeobacterium, Sulfolobus acidocaldarius.";
RL J. Biol. Chem. 265:21509-21513(1990).
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -!- SUBUNIT: Sul-ATPase is composed of six (or maybe five) subunits:
CC alpha, beta, delta, gamma, C (proteolipid), and possibly epsilon.
CC -!- SIMILARITY: Some, to E.hirae Ntph.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF000986; BAB66506.1; --
KW Complete proteome; Hydrogen ion transport; Hydrolase.
SQ SEQUENCE 59 AA; 7038 MW; 4C07944C732225D4 CRC64;

Query Match 14.3%; Score 53.5; DB 1; Length 59;
Best Local Similarity 30.6%; Pred. No. 6.6e+02;
Matches 22; Conservative 14; Mismatches 17; Indels 19; Gaps 5;

QY 7 DLDKSDVSLIFLMKDYMGKISKEKSFIDLVELEKLNL-----VAPQDLLEKLN 62
DB 3 EIDKSTIDKYINLK-----SKLDQKKNEL-----LSKINMEYEKTKQRLDELEKLN 52
QY 63 IHRIDIKTKIQK 74
DB 53 I-----LK-EVQK 59

RESULT 6
O9KEH2 PRELIMINARY; PRT; 48 AA.
AC O9KEH2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE BH0880 protein.
GN OrderedLocusNames=BH0880;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C-125;
RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AF001510; BAB04599.1; --
DR FIR; H83759; H83759.
KW Complete proteome.
SQ SEQUENCE 48 AA; 5625 MW; CA22B6E9AD436AC0 CRC64;

Query Match 14.2%; Score 53; DB 2; Length 48;
Best Local Similarity 41.3%; Pred. No. 6e+02;
Matches 19; Conservative 6; Mismatches 11; Indels 10; Gaps 2;

QY 24 MGRGKISKEKSFIDLVELEKLNLVAPDLDLEKLNHTRIDLK 69
DB 1 MGR-----KLLSFEELVLENKLLNDPEQLSKIEK-----RLDEK 36

RESULT 5
MTPE SULTO STANDARD; PRT; 59 AA.
AC P62019; P23039;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Membrane-associated ATPase epsilon chain (EC 3.6.3.14) (Sul-ATPase
DE epsilon chain).
GN Name=atpE; OrderedLocusNames=STI1438.1; ORFNames=STSI172;
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
SEQUENCE FROM N.A.
RX STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
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RA Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL; AB014316; AAN28970.1; -.
DR TIGR; BR0012; -.
KW Complete proteome.
SQ SEQUENCE 66 AA; 7674 MW; FC12C02001F514AE CRC64;

Query Match 14.2%; Score 53; DB 2; Length 66;
Best Local Similarity 48.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 5; Mismatches 4; Indels 4; Gaps 1;

QY 40 VELEKLNLV---APDQLDLLEKCL 60
DB 24 IELEDLDLVLSRIGPVDLDLMQEC 48

RESULT 9
Q7RS48 PRELIMINARY; PRT; 73 AA.
AC Q7RS48;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Hypothetical protein.
GN Name=PY00517;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368665; DOI=10.1038/nature01099;
RA Carlton J.M., Anguoli S.V., Suh B.B., Kooij T.W., Perteza M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01000144; EAA16610.1; -.
DR InterPro; IPR001388; Synaptobrevin.
DR PROSITE; PS50892; V SNARE; 1.
KW Hypothetical protein.
SQ SEQUENCE 73 AA; 8662 MW; BFE61FC8FB7D6527 CRC64;

Query Match 14.2%; Score 53; DB 2; Length 73;
Best Local Similarity 26.4%; Pred. No. 9.2e+02;
Matches 14; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

QY 19 LMKDYMGKISKSEKSFDLVVLEKLNIVAPDQLDLLEKCLNTHRIDLTKY 71
DB 1 MKRTLNLNCKCKDEKILAVKQKLNKINSVMNHNIDKLYESRGKIKALQYKTE 53

RESULT 10
O86256 PRELIMINARY; PRT; 51 AA.
ID O86256;
AC O86256;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 26, Last annotation update)
DE Leucine responsive element (fragment).

RA Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL; AB014316; AAN28970.1; -.
DR TIGR; BR0012; -.
KW Complete proteome.
SQ SEQUENCE 66 AA; 7674 MW; FC12C02001F514AE CRC64;

Query Match 14.2%; Score 53; DB 2; Length 66;
Best Local Similarity 48.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 5; Mismatches 4; Indels 4; Gaps 1;

QY 40 VELEKLNLV---APDQLDLLEKCL 60
DB 24 IELEDLDLVLSRIGPVDLDLMQEC 48

RESULT 9
Q7RS48 PRELIMINARY; PRT; 73 AA.
AC Q7RS48;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Hypothetical protein.
GN Name=PY00517;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368665; DOI=10.1038/nature01099;
RA Carlton J.M., Anguoli S.V., Suh B.B., Kooij T.W., Perteza M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01000144; EAA16610.1; -.
DR InterPro; IPR001388; Synaptobrevin.
DR PROSITE; PS50892; V SNARE; 1.
KW Hypothetical protein.
SQ SEQUENCE 73 AA; 8662 MW; BFE61FC8FB7D6527 CRC64;

Query Match 14.2%; Score 53; DB 2; Length 64;
Best Local Similarity 29.9%; Pred. No. 8.1e+02;
Matches 20; Conservative 14; Mismatches 13; Indels 20; Gaps 4;

QY 1 MARI-GEDLDKSVSLIFMK-----DYMGRGKISKSEKSFDLVVLEKLNIVA 49
DB 1 MARIKYEINDVNLIDYLNKRYRVDRIWVDY--NGDIVKSDP-----EKINIKN 51

QY 50 PQOLDLL 56
DB 52 TDKIEIV 58

RESULT 8
Q8G3D6 PRELIMINARY; PRT; 66 AA.
ID Q8G3D6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Hypothetical protein.
GN OrderedLocustNames=BR0012;
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kaul M., Shetty J., Malek J.A.,
RA Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
RA Salzberg S.L., Hoover D.L., Lindler L.E., Hailing S.M., Boyle S.M.,
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```
GN Name=lrp;
OS Klebsiella oxytoca
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=571;
RN [1]
RP SEQUENCE FROM N.A.
RA Albrecht C., Kleiner D.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y16963; CAA76565.1; -
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000485; HTH_AsnC_lrp.
DR InterPro; IPR009058; wing_hix_DNA_bnd.
DR PRINTS; PR00033; HTHASNC.
DR PROSITE; PS00956; HTH_ASN_C_2; 1.
FT NON_TER 51
SQ SEQUENCE 51 AA; 5857 MW; AE2B4C696F789F03 CRC64;

Query Match 13.9%; Score 52; DB 2; Length 51;
Best Local Similarity 32.8%; Pred. No. 8e+02;
Matches 20; Conservative 8; Mismatches 15; Indels 18; Gaps 3;

QY 5 GEDLDKSDVSSLIPLMKDYMGRGKISKESKSFLLDVVELEKLNIVAPDQLDLLEKCLKNIH 64
DB 9 GKDLDRIDRILNLELQD-----GRISN-----VELSKRVGLSP-----TPCLERVX 50

QY 65 R 65
DB 51 R 51

RESULT 11
ID Q813F1 PRELIMINARY; PRT; 51 AA.
AC Q813F1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical Cytosolic Protein.
GN OrderedLocusNames=BC3144;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelson B.,
RA Kapural V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis."
RL Nature 423:87-91(2003).
DR EMBL; AS017008; AAP10086.1; -
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 51 AA; 5923 MW; C811DB6E5E6DA468 CRC64;

Query Match 13.9%; Score 52; DB 2; Length 51;
Best Local Similarity 39.4%; Pred. No. 8e+02;
Matches 13; Conservative 8; Mismatches 10; Indels 2; Gaps 2;

QY 10 KSDVSSLI-FLMKDYMGRGKISKESKSFLLDVV 40
DB 9 ESEISKATHWEKDYLGSGISVKTILDRMII 41

RESULT 12
Q9RSY9
ID Q9RSY9 PRELIMINARY; PRT; 45 AA.
AC Q9RSY9;
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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE RNA polymerase sigma factor (Fragment).
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93294870; PubMed=7685830;
RA Kim C.W., Markiewicz P., Lee J.J., Schierle C.F., Miller J.H.;
RT "Studies of the hyperthermophile Thermotoga maritima by random
RT sequencing of cDNA and genomic libraries. Identification and
RT sequencing of the trpEG (D) operon."
RL J. Mol. Biol. 231:960-981(1993).
DR HSSP; Q9EZJ8; 1KU2.
DR GO; GO:0016987; F:sigma factor activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006352; P:transcription initiation; IEA.
DR InterPro; IPR007627; Sigma70_r2.
DR InterPro; IPR000943; Sigma70.
DR Pfam; PF04542; Sigma70_k2; 1.
DR PROSITE; PS00715; SIGMA70_1; 1.
FT NON_TER 1
FT NON_TER 45
SQ SEQUENCE 45 AA; 5049 MW; F8ED52EB456B12F5 CRC64;

Query Match 13.8%; Score 51.5; DB 2; Length 45;
Best Local Similarity 38.9%; Pred. No. 8e+02;
Matches 14; Conservative 6; Mismatches 11; Indels 5; Gaps 1;

QY 6 EDLDKSDVSSLIPLMKDYMGRGKISKESKSFLLDVE 41
DB 3 EKLITSNLRVLVSIKRYMGRG-----LSFQDLIQE 33

RESULT 13
Q63F79
ID Q63F79 PRELIMINARY; PRT; 67 AA.
AC Q63F79;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=BTZK0829;
OS Bacillus cereus ZK.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=288681;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZK;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU19413.1; -
KW Hypothetical protein.
SQ SEQUENCE 67 AA; 7984 MW; AF1B680BF6DECA13 CRC64;

Query Match 13.8%; Score 51.5; DB 2; Length 67;
Best Local Similarity 36.1%; Pred. No. 1.2e+03;
Matches 13; Conservative 10; Mismatches 8; Indels 5; Gaps 2;

QY 38 LVVELEKLNIVAPDQLDLLEK-CLKNIHRIIDLTKTI 72
DB 2 LILKVVMMKLEKQELLELAKICKEN-----DLSTKL 33

RESULT 14
Q6XD88
ID Q6XD88 PRELIMINARY; PRT; 65 AA.
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 13:06:14 ; Search time 160 Seconds
(without alignments)
181.294 Million cell updates/sec

Title: US-10-713-208-6_COPY_1_75

Perfect score: 373

Sequence: 1 MAEIGEDLDKSDVSSLIPLM.....LSKCLKNHRIIDLKTKIQKY 75

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1070894

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	20.1	55	2	AAY33287 Human FLI
2	63	16.9	27	2	AAY33286 Viral DED
3	63	16.9	27	2	AAY33289 Viral DED
4	61.5	16.5	64	6	AB99801 Amino aci
5	56	15.0	60	1	AAP71178 Bacillus
6	55	14.7	46	4	AAM16687 Peptide #
7	55	14.7	46	4	ABB35670 Peptide #
8	55	14.7	46	4	AAM29171 Peptide #
9	55	14.7	46	4	ABB30505 Peptide #
10	55	14.7	46	4	ABB21099 Protein #
11	55	14.7	46	4	AAM68864 Human bon
12	55	14.7	46	4	AAM56485 Human bon
13	55	14.7	46	4	ABG50524 Human liv
14	55	14.7	46	4	AAM04403 Peptide #
15	55	14.7	46	5	ABG38444 Human pep
16	54	14.5	49	4	AAM20621 Peptide #
17	54	14.5	49	4	ABB41825 Peptide #
18	54	14.5	49	4	AAM35621 Peptide #
19	54	14.5	49	4	ABB25545 Protein #
20	54	14.5	49	4	AAM75515 Human bon
21	54	14.5	49	4	AAM62697 Human bra
22	54	14.5	49	4	ABG57263 Human liv
23	54	14.5	49	5	ABG45071 Human pep
24	51.5	13.8	47	4	AAM09375 Staphyloc
25	51	13.7	47	4	AAM09373 Staphyloc

26	49.5	13.3	62	5	ABP33224 Human ORF
27	49.5	13.3	71	4	AM18411 Peptide #
28	49.5	13.3	71	4	ABB37453 Peptide #
29	49.5	13.3	71	4	AM30888 Peptide #
30	49.5	13.3	71	4	ABB32201 Peptide #
31	49.5	13.3	71	4	ABB22746 Protein #
32	49.5	13.3	71	4	AM70575 Human bon
33	49.5	13.3	71	4	AM58128 Human bra
34	49.5	13.3	71	4	ABG52254 Human liv
35	49.5	13.3	71	4	AM06010 Peptide #
36	49.5	13.3	71	5	ABG40238 Human pep
37	49	13.1	38	4	ABB37000 Peptide #
38	49	13.1	38	4	AM70140 Human bon
39	49	13.1	38	4	ABG51850 Human liv
40	49	13.1	53	4	AM17292 Peptide #
41	49	13.1	53	4	ABG51131 Human liv
42	49	13.1	53	4	AM04977 Peptide #
43	49	13.1	68	2	AAW77599 Staphyloc
44	48.5	13.0	30	2	AM45253 Peptide C
45	48.5	13.0	66	3	AG60317 Arabidops

ALIGNMENTS

RESULT 1
AAY33287
ID AAY33287 standard; peptide; 55 AA;

XX AAY33287;

XX DT 23-NOV-1999 (first entry)

XX DE Human FLICE DED peptide fragment.

XX KW DED; death effector domain; FLICE protein; screening; anti-HHV-6;
viral envelope; apoptosis; multiple sclerosis; immunodeficient;
central nervous system; infection.

XX OS Homo sapiens.

XX PN DE19812182-A1.

XX PD 23-SEP-1999.

XX PF 19-MAR-1998; 98DE-01012182.

XX PR 19-MAR-1998; 98DE-01012182.

XX PA (FARB) BAYER AG.

XX PI Weber O, Hug H;

XX DR WPI; 1999-528902/45.

XX PT Identifying substances with anti-human herpes virus 6 activity useful for
treating multiple sclerosis and infections of the central nervous system.
Disclosure; Page 3; 4pp; German.

XX CC This invention describes a novel method to screen for effective anti-HHV-
6 compounds which comprises incubating Fas-primed cells transfected with
human herpes virus 6 (HHV-6) viral envelope or fragments of the viral
envelope with putative anti-HHV-6 compounds and examining the apoptotic
behaviour of the cells. The method is used to identify new anti-human
herpes virus 6 compounds, targeted to a death effector domain (DED)-
homologous region in HHV. These are effective for treating multiple
sclerosis and infections of the central nervous system, especially in
immunodeficient patients. This sequence represents a human FLICE protein
DED region which is used to describe the method of the invention

XX Sequence 55 AA;

SQ


```
PA (INSP ) INST PASTEUR.
XX Drulhe P, Gruener A;
XX
XX WPI; 2003-129263/12.
XX N-PSDB; AB223335.
XX
XX New polynucleotide from Plasmodium falciparum and derived protein, useful
XX as immunogen for antimalarial vaccines and for preparing diagnostic or
XX therapeutic antibodies.
XX
XX Claim 5; Fig 1C; 115pp; French.
XX
XX The present sequence is a Plasmodium falciparum antigen, designated
XX Dc747. This antigen generates an interferon-gamma response. The protein
XX is localised on the surface of sporozoites and on the intra-hepatic stage
XX of parasites. The antigen, as well as nucleic acids encoding it, is
XX useful as immunogens/vaccines for protection against infection by
XX Plasmodium falciparum. They are useful in treating P. falciparum malaria
XX and for in vitro diagnosis of infection
XX
XX Sequence 64 AA;

Query Match 16.5%; Score 61.5; DB 6; Length 64;
Best Local Similarity 30.5%; Pred. No. 18;
Matches 18; Conservative 13; Mismatches 21; Indels 7; Gaps 2;

QY 18 FLMKDYMGKGI---SKEKSFLDLVVELEKLNLVAPDQDLLEKCLKNHRIIDLKTKIQ 73
DB 2 FHMHDYIDRIYNDKKN---VKSNDKNVKSNDKNVKSNDKNVKSNDKNVKSNDKNV 56

RESULT 5
AAP711178
ID AAP711178 standard; protein; 60 AA.
AC AAP711178;
XX
XX 25-MAR-2003 (revised)
DT 10-MAR-2003 (revised)
DT 15-APR-1991 (first entry)
XX
XX Bacillus exoprotease secretion promoting protein.
DE
XX
XX Exoprotease.
KW
XX
XX Bacillus sp.
OS
XX
XX JP61282400-A.
PN
XX
XX 12-DEC-1986.
PD
XX
XX 07-JUN-1985; 85JP-00123736.
PF
XX
XX 07-JUN-1985; 85JP-00123736.
PR
XX
XX (MITU ) MITSUBISHI CHEM IND LTD.
PA
XX
XX WPI; 1987-025820/04.
DR
XX
XX N-PSDB; AAN71310.
DR
XX
XX Protein promoting extra:cellular prodn. of exo:protease - by use of
XX recombinant DNA technique.
PT
XX
XX Claim 3; Page 1060; 8pp; Japanese.
PS
XX
XX Protein may be produced from a bacterial expression vector, and has
XX extracellular exoprotease production promoting activity. (Updated on 10-
XX MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA
XX field.)
XX
XX Sequence 60 AA;

Query Match 15.0%; Score 56; DB 1; Length 60;
Best Local Similarity 27.8%; Pred. No. 72;
Matches 15; Conservative 14; Mismatches 17; Indels 8; Gaps 1;

QY 28 KISKEKSFLDLVVELEKLNLVAPDQDLLEK-----CLKNHRIIDLKTKIQ 73
DB 7 KLJLHKTFFIEIYSDLEELADIAGKKGKPSMEKYVEIEQRCKQNILAEIQMKIK 60

RESULT 6
AAM16687
ID AAM16687 standard; protein; 46 AA.
XX
XX AAM16687;
AC
XX
XX 12-OCT-2001 (first entry)
DT
XX
XX Peptide #3121 encoded by probe for measuring cervical gene expression.
DE
XX
XX Probe; human; microarray; gene expression; cervical epithelial cell;
KW
XX
XX cervical cancer.
KW
XX
XX Homo sapiens.
OS
XX
XX WO200157278-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US000670.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR
XX
XX 26-MAY-2000; 2000US-0207456P.
PR
XX
XX 03-JUN-2000; 2000US-00608408.
PR
XX
XX 03-AUG-2000; 2000US-00632366.
PR
XX
XX 21-SEP-2000; 2000US-0234687P.
PR
XX
XX 27-SEP-2000; 2000US-0236359P.
PR
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX
XX WPI; 2001-488901/53.
DR
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human cervical epithelial cells.
PT
XX
XX Claim 27; SEQ ID NO 21513; 487pp; English.
PS
XX
XX The present invention relates to human single exon nucleic acid probes
XX (SENP: see AAI10068-AA128459). The present sequence is a peptide encoded
XX by one such probe. The SENPs are derived from human Hela cells. The SENPs
XX can be used to produce a single exon microarray, which can be used for
XX measuring human gene expression in a sample derived from human cervical
XX epithelial cells. By measuring gene expression, the probes are therefore
XX useful in grading and/or staging of diseases of the cervix, notably
XX cervical cancer. Note: The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 46 AA;

Query Match 14.7%; Score 55; DB 4; Length 46;
Best Local Similarity 30.6%; Pred. No. 69;
Matches 11; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 34 SFIDLVELEKLNLVAPDQDLLEKCLKNHRIIDLK 69
DB 1 NLLDPIEMERKRVILGEGKLDILKRVCAQINKSLK 36

RESULT 7
ABB35670
```


Penn SG, Hanzel DK, Chen W, Rank DR;
WPI; 2001-496933/54.
New spatially-addressable set of single exon nucleic acid probes, useful
for measuring gene expression in sample derived from human breast,
comprises number of single exon nucleic acid probes.

Claim 27; SEQ ID NO 13473; 327pp + Sequence Listing; English.

The invention relates to a spatially-addressable set of single exon
nucleic acid probes for measuring gene expression in a sample derived
from human breast and Br 474 cells. The method involves contacting the
probes with a collection of detectably labelled nucleic acids derived
from mRNA of human breast, and then measuring the label bound to each
probe of the microarray. The probes are useful for verifying the
expression of regions of genomic DNA predicted to encode proteins. They
are useful for gene discovery, and for determining predisposition and/or
prognosing breast disease. Gene expression analysis is useful for
assessing the toxicity of chemical agents on cells. The microarray of
this invention presents a far greater diversity of probes for measuring
gene expression, with far less bias than expressed sequence tag
microarrays. The method is suitable for rapid production of functional
information from genomic sequence. The present sequence is a peptide
encoded by a single exon nucleic acid probe of the invention. Note: The
sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences

Sequence 46 AA;

Query Match 14.7%; Score 55; DB 4; Length 46;
Best Local Similarity 30.6%; Pred. No. 69;
Matches 11; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 34 SFGLDVLVELEKLNVPADQLDLLEKLCNKNIHRIDLK 69
: ||| :||| :: :|||:: :|||
Db 1 NLLDFIEMEKRVILGEGKLDKLRVCAQINKSLIK 36

RESULT 10
ABB21099
ID ABB21099 standard; protein; 46 AA.
AC ABB21099;
XX
XX 23-JAN-2002 (first entry)
DE Protein #3098 encoded by probe for measuring heart cell gene expression.
KW Human; gene expression; heart; microarray; vascular system;
cardiovascular disease; hypertension; cardiac arrhythmia;
congenital heart disease.
OS Homo sapiens.
PN WO200157274-A2.
XX
PD 09-AUG-2001.
PF 30-JAN-2001; 2001WO-US000666.
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;

Penn SG, Hanzel DK, Chen W, Rank DR;
WPI; 2001-488999/53.
Single exon nucleic acid probes for analyzing gene expression in human
hearts.

Claim 15; SEQ ID NO 22869; 530pp; English.

The present invention relates to single exon nucleic acid probes for
measuring human gene expression in a sample derived from human heart (see
ABA21535-ABAA41305). The present sequence is a protein encoded by one such
probe. The probes may be used for predicting, measuring and displaying
gene expression in samples derived from the human heart via microarrays.
By measuring gene expression, the probes are useful for predicting,
diagnosing, grading, staging, monitoring and prognosing diseases of the
human heart and vascular system e.g. cardiovascular disease,
hypertension, cardiac arrhythmias and congenital heart disease. Note: The
sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences

Sequence 46 AA;

Query Match 14.7%; Score 55; DB 4; Length 46;
Best Local Similarity 30.6%; Pred. No. 69;
Matches 11; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 34 SFGLDVLVELEKLNVPADQLDLLEKLCNKNIHRIDLK 69
: ||| :||| :: :|||:: :|||
Db 1 NLLDFIEMEKRVILGEGKLDKLRVCAQINKSLIK 36

RESULT 11
AAM68864
ID AAM68864 standard; protein; 46 AA.
XX
AC AAM68864;
DT 06-NOV-2001 (first entry)
XX
XX Human bone marrow expressed probe encoded protein SEQ ID NO: 29170.
DE Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
KW
XX Homo sapiens.
XX
XX WO200157276-A2.
PN
XX 09-AUG-2001.
PD
XX 30-JAN-2001; 2001WO-US000668.
PP
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
WPI; 2001-488999/53.
Human genome-derived single exon nucleic acid probes useful for analyzing
gene expression in human bone marrow.

Example 4; SEQ ID NO 29170; 658pp + Sequence Listing; English.

The present invention provides a number of single exon nucleic acid

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 13:22:45 ; Search time 155 Seconds
(without alignments)
185.797 Million cell updates/sec

Title: US-10-713-208-6_COPY_1_75

Perfect score: 373

Sequence: 1 MAEIGEDLDKSDVSSLIFLM.....LEKCLKNIHRIDLTQIKY 75

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 635259

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	277	74.3	56	15	US-10-627-571-5 Sequence 5, Appli
2	277	74.3	56	15	US-10-627-571-7 Sequence 7, Appli
3	237	63.5	56	15	US-10-627-571-6 Sequence 6, Appli
4	225.5	60.5	59	15	US-10-627-571-4 Sequence 4, Appli
5	99	26.5	75	14	US-10-001-254-31 Sequence 31, Appl
6	90	24.1	75	9	US-09-952-768-66 Sequence 66, Appl
7	90	24.1	75	15	US-10-668-955-66 Sequence 66, Appl
8	79	21.2	56	15	US-10-627-571-9 Sequence 9, Appli
9	74	19.8	72	14	US-10-001-254-34 Sequence 34, Appl
10	68	18.2	56	15	US-10-627-571-8 Sequence 8, Appli
11	61.5	16.5	64	17	US-10-712-533A-3 Sequence 3, Appli

12	60	16.1	50	16	US-10-776-013-436 Sequence 436, App
13	56	15.0	57	17	US-10-489-123-13 Sequence 13, Appl
14	55	14.7	40	17	US-10-489-123-14 Sequence 14, Appl
15	55	14.7	46	9	US-09-864-761-36397 Sequence 36397, A
16	54	14.5	49	9	US-09-864-761-40843 Sequence 40843, A
17	53.5	14.3	72	17	US-10-489-123-12 Sequence 12, Appl
18	53	14.2	73	16	US-10-437-963-169508 Sequence 169508, A
19	52.5	14.1	66	15	US-10-627-571-3 Sequence 3, Appli
20	52	13.9	65	15	US-10-424-599-164893 Sequence 164893, A
21	52	13.9	68	16	US-10-425-115-185640 Sequence 185640, A
22	52	13.9	70	15	US-10-424-599-244882 Sequence 244882, A
23	51.5	13.8	47	9	US-09-823-266-15 Sequence 15, Appl
24	51.5	13.8	47	14	US-10-155-419-15 Sequence 15, Appl
25	51	13.7	47	9	US-09-823-266-13 Sequence 13, Appl
26	51	13.7	47	14	US-10-155-419-13 Sequence 13, Appl
27	50	13.4	53	15	US-10-424-599-181787 Sequence 181787, A
28	50	13.4	59	15	US-10-335-977-8130 Sequence 8130, Ap
29	49.5	13.3	62	11	US-09-864-408A-4394 Sequence 4394, A
30	49.5	13.3	71	9	US-09-864-761-38044 Sequence 38044, A
31	49.5	13.3	75	16	US-10-767-701-50523 Sequence 50523, A
32	49	13.1	38	9	US-09-864-761-46700 Sequence 46700, A
33	49	13.1	53	9	US-09-864-761-46621 Sequence 46621, A
34	49	13.1	68	9	US-09-939-980-359 Sequence 359, App
35	49	13.1	71	16	US-10-437-963-183337 Sequence 183337, A
36	49	13.1	72	16	US-10-425-115-241056 Sequence 241056, A
37	48.5	13.0	66	9	US-09-815-242-11591 Sequence 11591, A
38	48.5	13.0	68	16	US-10-767-701-55846 Sequence 55846, A
39	48	12.9	50	17	US-10-690-276-570 Sequence 570, App
40	48	12.9	54	15	US-10-627-571-19 Sequence 19, Appl
41	48	12.9	66	16	US-10-856-499-1915 Sequence 1915, Ap
42	48	12.9	72	16	US-10-437-963-168063 Sequence 168063, A
43	47.5	12.7	47	9	US-09-823-266-14 Sequence 14, Appl
44	47.5	12.7	47	14	US-10-155-419-14 Sequence 14, Appl
45	47.5	12.7	51	14	US-10-097-065-620 Sequence 620, App

ALIGNMENTS

RESULT 1

US-10-627-571-5
; Sequence 5, Application US/10627571
; Publication No. US20040082771A1
; GENERAL INFORMATION:
; APPLICANT: KASID, Usha N.
; APPLICANT: KUMAR, Deepak
; APPLICANT: GOKHALE, Prafulla
; APPLICANT: AHMAD, Imran
; TITLE OF INVENTION: ANTI-APOTOPIC GENE SCC-S2 AND DIAGNOSTIC AND THERAPEUTIC USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 223316
; CURRENT APPLICATION NUMBER: US/10/627,571
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/264,062
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: PCT/US02/02212
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ IDS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: CASH Alpha/Beta - fragment
US-10-627-571-5

Query Match 74.3%; Score 277; DB 15; Length 56;
Best Local Similarity 100.0%; Pred. No. 46-24;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 SDVSSLIPLMKDYNMGKISKEKSFLLDVVELEKLNVLVAPDQDLLEKCLKNIHRI 66

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Db      1 SDVSSLIFLMKDYMGKGKSKSEKSFDDLVLVELEKLNLVAPDQDLDLLEKCLKNIHRI 56
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RESULT 2
US-10-627-571-7
; Sequence 7, Application US/10627571
; Publication No. US20040082771A1
; GENERAL INFORMATION:
; APPLICANT: KASID, Usha N.
; APPLICANT: KUMAR, Deepak
; APPLICANT: GOKHALE, Prafulla
; APPLICANT: AHMAD, Imran
; TITLE OF INVENTION: ANTI-APOTOPIC GENE SCC-S2 AND DIAGNOSTIC AND THERAPEUTIC USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 223316
; CURRENT APPLICATION NUMBER: US/10/627,571
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/264,062
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: PCT/US02/02212
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 7
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: FLIP (L) - fragment
US-10-627-571-7

Query Match      74.3%; Score 277; DB 15; Length 56;
Best Local Similarity 100.0%; Pred. No. 4e-24; Indels 0; Gaps 0;
Matches 56; Conservative 0; Mismatches 0;

QY      11 SDVSSLIFLMKDYMGKGKSKSEKSFDDLVLVELEKLNLVAPDQDLDLLEKCLKNIHRI 66
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Db      1 SDVSSLIFLMKDYMGKGKSKSEKSFDDLVLVELEKLNLVAPDQDLDLLEKCLKNIHRI 56
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RESULT 3
US-10-627-571-6
; Sequence 6, Application US/10627571
; Publication No. US20040082771A1
; GENERAL INFORMATION:
; APPLICANT: KASID, Usha N.
; APPLICANT: KUMAR, Deepak
; APPLICANT: GOKHALE, Prafulla
; APPLICANT: AHMAD, Imran
; TITLE OF INVENTION: ANTI-APOTOPIC GENE SCC-S2 AND DIAGNOSTIC AND THERAPEUTIC USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 223316
; CURRENT APPLICATION NUMBER: US/10/627,571
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/264,062
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: PCT/US02/02212
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 6
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: FLIP (L) - fragment
US-10-627-571-6

Query Match      63.5%; Score 237; DB 15; Length 56;
Best Local Similarity 80.4%; Pred. No. 1.5e-19;
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Matches 45; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY      11 SDVSSLIFLMKDYMGKGKSKSEKSFDDLVLVELEKLNLVAPDQDLDLLEKCLKNIHRI 66
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Db      1 NDVSSLVFLTRDYGKGKIAKDKSFDDLVLVIELEKLNLIASDQNLLEKCLKNIHRI 56
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RESULT 4
US-10-627-571-4
; Sequence 4, Application US/10627571
; Publication No. US20040082771A1
; GENERAL INFORMATION:
; APPLICANT: KASID, Usha N.
; APPLICANT: KUMAR, Deepak
; APPLICANT: GOKHALE, Prafulla
; APPLICANT: AHMAD, Imran
; TITLE OF INVENTION: ANTI-APOTOPIC GENE SCC-S2 AND DIAGNOSTIC AND THERAPEUTIC USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 223316
; CURRENT APPLICATION NUMBER: US/10/627,571
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/264,062
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: PCT/US02/02212
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: CASH Alpha/Beta - fragment
US-10-627-571-4

Query Match      60.5%; Score 225.5; DB 15; Length 59;
Best Local Similarity 76.3%; Pred. No. 3.2e-18;
Matches 45; Conservative 8; Mismatches 3; Indels 3; Gaps 1;

QY      11 SDVSSLIFL---MKDYMGRGKSKSEKSFDDLVLVELEKLNLVAPDQDLDLLEKCLKNIHRI 66
|||||
Db      1 NDVSSLVFLTRDYGKGKIAKDKSFDDLVLVIELEKLNLIASDQNLLEKCLKNIHRI 59
|||||
RESULT 5
US-10-001-254-31
; Sequence 31, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sug Hyung
; APPLICANT: Roth, Wilfred
; APPLICANT: Stenner-Liewen, Frank
; TITLE OF INVENTION: No US20030049702A1el Death Domain Proteins
; FILE REFERENCE: P-LJ 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-254-31
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Db 66 INRLDL 71


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; APPLICANT: Bartel, Paul
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND
; TITLE OF INVENTION: DISBASES
; FILE REFERENCE: 1600.24
; CURRENT APPLICATION NUMBER: US/10/776,013
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 09/948904
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 09/466139
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/113534
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/124120
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/141243
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/975072
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 10/194967
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 60/304775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 695
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 436
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-776-013-436

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Query Match 16.1%; Score 60; DB 16; Length 50;
Best Local Similarity 31.8%; Pred. No. 20;
Matches 14; Conservative 12; Mismatches 14; Indels 4; Gaps 1;

[illegible]

RESULT 13
US-10-489-123-13
; Sequence 13, Application US/10489123
; Publication No. US20050074463A1

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; GENERAL INFORMATION:
; APPLICANT: AUTRAN, BRIGITTE
; APPLICANT: SAMRI, ASSIA
; APPLICANT: DEBRE, PATRICE
; APPLICANT: CALVEZ, VINCENT
; APPLICANT: KATLAMA, CHRISTINE
; APPLICANT: HAAS, GABY
; TITLE OF INVENTION: THERAPEUTIC VACCINATION METHOD, MUTATED PEPTIDES OF HIV
; TITLE OF INVENTION: REVERSE TRANSCRIPTASE AND THEIR USE FOR VACCINATION AND
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; FILE REFERENCE: BDAC:007US
; CURRENT APPLICATION NUMBER: US/10/489,123
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: PCT/FR01/02872
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-489-123-13

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Query Match 15.0%; Score 56; DB 17; Length 57;

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Best Local Similarity 31.9%; Pred. No. 68;
Matches 15; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

QY      1  MAEIGEDLDKS---DVSSLIFLMKDYMGKGIKSEKSFLLDVVELEK 44
      ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      5  LVEICAELEKEGKISIKALVEICAELEKEGKISK-KALVEICAELEK 50

RESULT 14
US-10-489-123-14
; Sequence 14, Application US/10489123
; Publication No. US20050074463A1
; GENERAL INFORMATION:
; APPLICANT: AUTRAN, BRIGITTE
; APPLICANT: SAMRI, ASSIA
; APPLICANT: DEBRE, PATRICE
; APPLICANT: CALVEZ, VINCENT
; APPLICANT: KATLAMA, CHRISTINE
; APPLICANT: HAAS, GABY
; TITLE OF INVENTION: THERAPEUTIC VACCINATION METHOD, MUTATED PEPTIDES OF HIV
; TITLE OF INVENTION: REVERSE TRANSCRIPTASE AND THEIR USE FOR VACCINATION AND
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; FILE REFERENCE: BDAC:007US
; CURRENT APPLICATION NUMBER: US/10/489,123
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: PCT/FR01/02872
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-489-123-14

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Query Match 14.7%; Score 55; DB 17; Length 40;
Best Local Similarity 34.4%; Pred. No. 59;
Matches 11: Conservative 9; Mismatches 12; Indels

Qy	13	VSSLI	FLMKD	YMG	RKISKE	SFLDL	VVELEK	44
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Db	2	IKALVEI	CAELEKE	GKISKI	KALVEI	CAELEK	33	

RESULT 15
US-09-864-761-36397
; Sequence 36397, Application US/09864761
; Patent No. US2002048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,365
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36397
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007256.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.5
; OTHER INFORMATION: EST HUMAN HIT: BF095670.1, EVALUE 9.00e-19
; OTHER INFORMATION: SWISSPROT HIT: Q14790, EVALUE 7.00e-20
US-09-864-761-36397

Query Match 14.7%; Score 55; DB 9; Length 46;
Best Local Similarity 30.6%; Pred. No. 69;
Matches 11; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 34 SFLLDLVVELEKLNVLAPDQDLLEKCLKNIHRIDLK 69
Db 1 NLLDIFIEMEKRVILGEGKLDILKRVCAQINKSLK 36

Search completed: June 20, 2005, 13:38:15
Job time : 156 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2005, 13:19:14 ; Search time 42 Seconds
(without alignments)
133.302 Million cell updates/sec

Title: US-10-713-208-6_COPY_1_75

Perfect score: 373

Sequence: 1 MAEIGBLLDKSDVSSLIPLM.....LEKCLKNIHRIDLTKYIKRY 75

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 302356

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A COMB pep.*
- 2: /cgn2_6/prodata/1/iaa/5B COMB pep.*
- 3: /cgn2_6/prodata/1/iaa/6A COMB pep.*
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- 5: /cgn2_6/prodata/1/iaa/PCUTUS COMB pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1 pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	99	26.5	75	1	US-08-665-220-66
2	91	24.4	68	4	US-09-180-167A-13
3	91	24.4	68	4	US-09-033-524B-13
4	90	24.1	75	3	US-09-291-692-66
5	90	24.1	75	4	US-09-952-768-66
6	80	21.4	66	4	US-09-180-167A-12
7	80	21.4	66	4	US-09-033-524B-12
8	69	18.5	64	4	US-09-180-167A-31
9	69	18.5	64	4	US-09-033-524B-31
10	66	17.7	67	4	US-09-180-167A-10
11	66	17.7	67	4	US-09-033-524B-10
12	51.5	13.8	47	4	US-09-823-266-15
13	51	13.7	47	4	US-09-823-266-13
14	51	13.7	47	4	US-09-180-167A-11
15	51	13.7	47	4	US-09-033-524B-11
16	50.5	13.5	69	4	US-09-621-976-7353
17	49	13.1	54	4	US-09-621-976-4976
18	49	13.1	68	3	US-08-936-165A-359
19	49	13.1	72	4	US-09-621-976-7354
20	48.5	13.0	70	3	US-09-367-953B-107
21	48.5	13.0	72	4	US-09-270-767-32287
22	48.5	13.0	72	4	US-09-270-767-47504
23	48	12.9	66	4	US-09-640-211A-1915
24	48	12.9	67	2	US-08-142-551B-9
25	47.5	12.7	47	4	US-09-823-266-14
26	47	12.6	66	2	US-08-867-087B-40
27	46	12.3	41	3	US-08-974-549A-181

28 46 12.3 41 4 US-09-402-181B-181 Sequence 181, App
29 46 12.3 41 4 US-09-721-456-181 Sequence 181, App
30 46 12.3 49 3 US-09-382-155-4 Sequence 4, Appli
31 46 12.3 49 3 US-09-074-044A-4 Sequence 4, Appli
32 46 12.3 61 4 US-09-248-796A-25750 Sequence 25750, A
33 46 12.3 71 4 US-09-248-796A-24519 Sequence 24519, A
34 45.5 12.2 73 4 US-09-125-635-3 Sequence 3, Appli
35 45 12.1 68 4 US-09-270-767-40620 Sequence 40620, A
36 45 12.1 68 4 US-09-270-767-55836 Sequence 55836, A
37 44.5 11.9 34 4 US-09-843-221A-89 Sequence 89, Appl
38 44.5 11.9 66 4 US-09-732-210-829 Sequence 829, App
39 44.5 11.9 70 4 US-09-543-681A-7547 Sequence 7547, Ap
40 44.5 11.9 75 3 US-08-858-207A-460 Sequence 460, App
41 44 11.8 35 3 US-09-082-279B-276 Sequence 276, App
42 44 11.8 35 3 US-09-082-279B-277 Sequence 277, App
43 44 11.8 35 3 US-09-315-304B-276 Sequence 276, App
44 44 11.8 35 3 US-09-315-304B-277 Sequence 277, App
45 44 11.8 35 4 US-09-834-784-276 Sequence 276, App

ALIGNMENTS

RESULT 1
US-08-665-220-66
Sequence 66, Application US/08665220
Patent No. 5786173
GENERAL INFORMATION:
APPLICANT: Alnemti, Emad S.
APPLICANT: Fernandes-Alnemti, Teresa
APPLICANT: Litwack, Gerald
APPLICANT: Armstrong, Robert
APPLICANT: Tomaseilli, Kevin
TITLE OF INVENTION: Mch4 and Mch5, Apoptotic Proteases,
TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,220
FILING DATE: 14-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/618,408
FILING DATE: 19-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2165
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..75
OTHER INFORMATION: /note="Mch5 A"
US-08-665-220-66

; TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,
; NUCLEIC ACIDS ENCODING AND METHODS OF USE

; NUMBER OF SEQUENCES: 75

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed Intellectual Property Law Group

; STREET: Suite 6300, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/952,768

; FILING DATE: 10-Sep-2001

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Christiansen, William T.

; REGISTRATION NUMBER: 44,614

; REFERENCE/DOCKET NUMBER: 480140.424C4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 66:

; SEQUENCE CHARACTERISTICS:

; TYPE: amino acid

; LENGTH: 75 amino acids

; STRANDEDNESS: <Unknown>

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 1..75

; OTHER INFORMATION: /note= "Mch5 A"

; SEQUENCE DESCRIPTION: SEQ ID NO: 66:

US-09-952-768-66

Query Match 24.1%; Score 90; DB 4; Length 75;

Best Local Similarity 34.8%; Pred. No. 0.00081;

Matches 23; Conservative 13; Mismatches 30; Indels 0; Gaps 0;

QY 3 EIGEDLDKSDVSSLIPLMKDYMGRGKISKEKSFGLDLVVELEKLNVLVAPDQDLLEKCLN 62

DB 6 DIGEQDSEDLSLKLFLSDYIPQRKQEPKDALMLFQRLQEKRMLEESNLSFLKELLR 65

QY 63 IHRIDL 68

DB 66 INRLDL 71

RESULT 6

US-09-180-167A-12

; Sequence 12, Application US/09180167A

; Patent No. 6558950

; GENERAL INFORMATION:

; APPLICANT: Gordon C. Shore et al.

; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING

; FILE REFERENCE: 50013/004003

; CURRENT APPLICATION NUMBER: US/09/180,167A

; CURRENT FILING DATE: 1999-09-10

; PRIOR APPLICATION NUMBER: CA 2,198,988

; PRIOR FILING DATE: 1997-03-03

; PRIOR APPLICATION NUMBER: PCT/IB98/00706

; PRIOR FILING DATE: 1998-03-02

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 12

; LENGTH: 66

; TYPE: PRT

; ORGANISM: Homo sapiens

Query Match 18.5%; Score 69; DB 4; Length 64;

Best Local Similarity 30.9%; Pred. No. 0.26;

Matches 17; Conservative 11; Mismatches 23; Indels 4; Gaps 1;

QY 3 EIGEDLDKSDVSSLIPLMKDYMGRGKISKEKSFGLDLVVELEKLNVLVAPDQDLLE 57

DB 11 ELSEGIDSENKDMIFLLKSLPK----TMTSLSFLAFLEKQKIDEDNLTCL 61

US-09-180-167A-12

Query Match

Best Local Similarity 21.4%; Score 80; DB 4; Length 66;

Matches 20; Conservative 11; Mismatches 27; Indels 0; Gaps 0;

QY 3 EIGEDLDKSDVSSLIPLMKDYMGRGKISKEKSFGLDLVVELEKLNVLVAPDQDLLEKCL 60

DB 9 DIGEQDSEDLSLKLFLSDYIPQRKQEPKDALMLFQRLQEKRMLEESNLSFLKELL 66

RESULT 7

US-09-033-524B-12

; Sequence 12, Application US/09033524B

; Patent No. 6607880

; GENERAL INFORMATION:

; APPLICANT: Gordon C. Shore et al.

; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING

; FILE REFERENCE: 50013/004002

; CURRENT APPLICATION NUMBER: US/09/033,524B

; CURRENT FILING DATE: 1998-03-02

; PRIOR APPLICATION NUMBER: CA 2,198,988

; PRIOR FILING DATE: 1997-03-03

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 12

; LENGTH: 66

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-033-524B-12

Query Match

Best Local Similarity 21.4%; Score 80; DB 4; Length 66;

Matches 20; Conservative 11; Mismatches 27; Indels 0; Gaps 0;

QY 3 EIGEDLDKSDVSSLIPLMKDYMGRGKISKEKSFGLDLVVELEKLNVLVAPDQDLLEKCL 60

DB 9 DIGEQDSEDLSLKLFLSDYIPQRKQEPKDALMLFQRLQEKRMLEESNLSFLKELL 66

RESULT 8

US-09-180-167A-31

; Sequence 31, Application US/09180167A

; Patent No. 6558950

; GENERAL INFORMATION:

; APPLICANT: Gordon C. Shore et al.

; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING

; FILE REFERENCE: 50013/004003

; CURRENT APPLICATION NUMBER: US/09/180,167A

; CURRENT FILING DATE: 1999-09-10

; PRIOR APPLICATION NUMBER: CA 2,198,988

; PRIOR FILING DATE: 1997-03-03

; PRIOR APPLICATION NUMBER: PCT/IB98/00706

; PRIOR FILING DATE: 1998-03-02

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 31

; LENGTH: 64

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-180-167A-31

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RESULT 9
US-09-033-524B-31
; Sequence 31, Application US/09033524B
; Patent No. 6607880
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
; TITLE OF INVENTION: APOPTOSIS
; FILE REFERENCE: 50013/004002
; CURRENT APPLICATION NUMBER: US/09/033,524B
; CURRENT FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: CA 2,198,988
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-033-524B-31

Query Match      18.5%; Score 69; DB 4; Length 64;
Best Local Similarity 30.9%; Pred. No. 0.26;
Matches 17; Conservative 11; Mismatches 23; Indels 4; Gaps 1;

QY      3  EIGEDLDKSDVSSLIPLMKDYMGRGKISKESFGLDLVVELEKLNLVAPDQDLLE 57
         |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      11  ELSEGIDSENKDMIFLLKDSLPK-----TMTSLSLFLAFLEKQKIDEDNLTCL 61

RESULT 10
US-09-180-167A-10
; Sequence 10, Application US/09180167A
; Patent No. 6558950
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
; TITLE OF INVENTION: APOPTOSIS
; FILE REFERENCE: 50013/004003
; CURRENT APPLICATION NUMBER: US/09/180,167A
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: CA 2,198,988
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: PCT/IB98/00706
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-167A-10

Query Match      17.7%; Score 66; DB 4; Length 67;
Best Local Similarity 29.8%; Pred. No. 0.65;
Matches 17; Conservative 13; Mismatches 27; Indels 0; Gaps 0;

QY      4  IGEDLDKSDVSSLIPLMKDYMGRGKISKESFGLDLVVELEKLNLVAPDQDLLEKCL 60
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Db      11  VSSLSSELTELKFLCLGRVGRKRLERVQSGLDLFSMLLEQNDLEPGHTELLRELL 67

RESULT 11
US-09-033-524B-10
; Sequence 10, Application US/09033524B
; Patent No. 6607880
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
; TITLE OF INVENTION: APOPTOSIS
; FILE REFERENCE: 50013/004002
; CURRENT APPLICATION NUMBER: US/09/033,524B
; CURRENT FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: US/09/033,524B
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-033-524B-10

Query Match      17.7%; Score 66; DB 4; Length 67;
Best Local Similarity 29.8%; Pred. No. 0.65;
Matches 17; Conservative 13; Mismatches 27; Indels 0; Gaps 0;

QY      4  IGEDLDKSDVSSLIPLMKDYMGRGKISKESFGLDLVVELEKLNLVAPDQDLLEKCL 60
         |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      11  VSSLSSELTELKFLCLGRVGRKRLERVQSGLDLFSMLLEQNDLEPGHTELLRELL 67

RESULT 12
US-09-823-266-15
; Sequence 15, Application US/09823266
; Patent No. 6613531
; GENERAL INFORMATION:
; APPLICANT: Burgess, Richard
; APPLICANT: Arthur, Terrance
; APPLICANT: Anthony, Larry
; APPLICANT: Bergendahl, Viet
; APPLICANT: Pietz, Bradley
; TITLE OF INVENTION: Sigma binding region of RNA polymerase and uses thereof
; FILE REFERENCE: 800.025US1
; CURRENT APPLICATION NUMBER: US/09/823,266
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,116
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 47
; TYPE: PRT
; ORGANISM: T. maritima
US-09-823-266-15

Query Match      13.8%; Score 51.5; DB 4; Length 47;
Best Local Similarity 38.9%; Pred. No. 26;
Matches 14; Conservative 6; Mismatches 11; Indels 5; Gaps 1;

QY      6  EDLDKSDVSSLIPLMKDYMGRGKISKESFGLDLVVE 41
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Db      8  EKLITSNLRVLVSVIAKRYMGRG-----LSFQDLIOE 38

RESULT 13
US-09-823-266-13
; Sequence 13, Application US/09823266
; Patent No. 6613531
; GENERAL INFORMATION:
; APPLICANT: Burgess, Richard
; APPLICANT: Arthur, Terrance
; APPLICANT: Anthony, Larry
; APPLICANT: Bergendahl, Viet
; APPLICANT: Pietz, Bradley
; TITLE OF INVENTION: Sigma binding region of RNA polymerase and uses thereof
; FILE REFERENCE: 800.025US1
; CURRENT APPLICATION NUMBER: US/09/823,266
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,116
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 47
; TYPE: PRT
; ORGANISM: T. maritima
US-09-823-266-13

Query Match      13.8%; Score 51.5; DB 4; Length 47;
Best Local Similarity 38.9%; Pred. No. 26;
Matches 14; Conservative 6; Mismatches 11; Indels 5; Gaps 1;

QY      6  EDLDKSDVSSLIPLMKDYMGRGKISKESFGLDLVVE 41
         |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      8  EKLITSNLRVLVSVIAKRYMGRG-----LSFQDLIOE 38
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Search completed: June 20, 2005, 13:34:31
Job time : 43 secs

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; ORGANISM: S. aureus
US-09-823-266-13

Query Match      13.7%; Score 51; DB 4; Length 47;
Best Local Similarity 31.0%; Pred. No. 30;
Matches 13; Conservative 11; Mismatches 8; Indels 10; Gaps 2;

QY 5 GEDLDKSDVS-----LIFLMKDYMGKGKISKEKSFDLVLVE 41
Db 2 GDEVAKSLAEANLRLVVSIAKRYVGRGML-----FLDLIQE 38

RESULT 14
US-09-180-167A-11
; Sequence 11, Application US/09180167A
; Patent No. 6558950
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
; TITLE OF INVENTION: APOPTOSIS
; FILE REFERENCE: 50013/004003
; CURRENT APPLICATION NUMBER: US/09/180,167A
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: CA 2,198,988
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: PCT/IB98/00706
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-180-167A-11

Query Match      13.7%; Score 51; DB 4; Length 67;
Best Local Similarity 28.3%; Pred. No. 46;
Matches 15; Conservative 12; Mismatches 26; Indels 0; Gaps 0;

QY 8 LDKSDVSSLIFLMKDYMGKGKISKEKSFDLVLVELEKLNLVAPQDLLEKCL 60
Db 15 LSGNDLMELKFLCRRVSKRKLRVQSGLDLFTVLLEQNDLERIGHTGLIRELL 67

RESULT 15
US-09-033-524B-11
; Sequence 11, Application US/09033524B
; Patent No. 6607880
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
; TITLE OF INVENTION: APOPTOSIS
; FILE REFERENCE: 50013/004002
; CURRENT APPLICATION NUMBER: US/09/033,524B
; CURRENT FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: CA 2,198,988
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-033-524B-11

Query Match      13.7%; Score 51; DB 4; Length 67;
Best Local Similarity 28.3%; Pred. No. 46;
Matches 15; Conservative 12; Mismatches 26; Indels 0; Gaps 0;

QY 8 LDKSDVSSLIFLMKDYMGKGKISKEKSFDLVLVELEKLNLVAPQDLLEKCL 60
Db 15 LSGNDLMELKFLCRRVSKRKLRVQSGLDLFTVLLEQNDLERIGHTGLIRELL 67

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 13:34:40 ; Search time 39 Seconds
(without alignments)
436.676 Million cell updates/sec

Title: US-10-713-208-6_COPY_76_252
Perfect score: 930
Sequence: 1 KQSVQAGSYRNVLQAAIQ.....YLAGPKMFFIQNVVSDGQ 177

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 89048

Minimum DB seq length: 0
Maximum DB seq length: 177

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: Pirl:.*
2: Pirl2:.*
3: Pirl3:.*
4: Pirl4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	73.5	7.9	149	2 T43637	caspase protein 1C
2	70.5	7.6	135	2 AE2322	hypothetical prote
3	69	7.4	152	2 A97355	hypothetical prote
4	68.5	7.4	136	2 T08216	outer arm dynein 1
5	68	7.3	137	1 JC4233	lysozyme (BC 3.2.1
6	67	7.2	125	2 AD0297	probable membrane
7	65.5	7.0	164	2 T16321	hypothetical prote
8	64.5	6.9	89	2 E47758	retrovirus-related
9	64.5	6.9	114	2 T17929	hypothetical prote
10	64.5	6.9	174	2 H31267	conserved hypotet
11	63.5	6.8	167	2 S34363	hypothetical prote
12	63.5	6.8	171	2 A11060	probable acetyltra
13	63	6.8	172	2 B82053	probable fibrillar
14	61.5	6.6	156	2 H86572	hypothetical prote
15	61.5	6.6	160	2 B82382	transcription regu
16	61	6.6	149	1 B69073	NADP-reducing hydr
17	61	6.6	160	2 H75062	flagella-related p
18	60.5	6.5	99	2 A70366	hypothetical prote
19	60	6.5	136	2 I51222	neurotrophin recept
20	60	6.5	157	2 S76052	hypothetical prote
21	59.5	6.4	154	2 F81917	hypothetical prote
22	59.5	6.4	156	2 T12893	hypothetical prote
23	58.5	6.3	120	2 E70479	dnak suppressor pr
24	58.5	6.3	146	2 A42258	hypothetical prote
25	58.5	6.3	153	2 A87732	protein W10C8.4 [i
26	58.5	6.3	157	2 S35486	xy1s protein - Pse
27	58.5	6.3	159	2 C97071	phosphoriboylecarb
28	58.5	6.3	165	2 AB2113	hypothetical prote
29	58	6.2	118	2 T14570	cytochrome b559 co

30	58	6.2	147	2 D69008	conserved hypotchet
31	58	6.2	175	2 B97314	probable transcript
32	57.5	6.2	160	1 B69186	conserved hypotchet
33	57	6.1	104	2 A12257	hypothetical prote
34	57	6.1	119	2 T25062	hypothetical prote
35	57	6.1	162	2 T40004	hypothetical prote
36	57	6.1	173	2 T48097	glutathione peroxi
37	56.5	6.1	150	2 B23253	myosin A2 catalyti
38	56.5	6.1	161	2 A44821	general odorant-bi
39	56.5	6.1	173	2 T19101	hypothetical prote
40	56	6.0	94	2 T38652	hypothetical prote
41	56	6.0	95	1 A69697	ribosomal protein
42	56	6.0	104	2 G64340	hypothetical prote
43	56	6.0	109	2 D70077	hypothetical prote
44	56	6.0	154	2 H97860	hypothetical prote
45	55.5	6.0	148	2 C71353	hypothetical prote

ALIGNMENTS

RESULT 1

T43637
caspase protein 1C - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43637
R:Shaham, S.
J. Biol. Chem. 273, 35109-35117, 1998
A:Title: Identification of multiple Caenorhabditis elegans caspases and their potential
A:Reference number: Z22587; MUID:99074291; PMID:9857046
A:Accession: T43637
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-149 <SHA>
A:Cross-references: UNIPROT:Q9Y056; EMBL:AF088287; NID:G4063371; PIDN:AAC98294.1; PID:G4063371
C:Genetics:
A:Note: csp-1

Query Match 7.9%; Score 73.5; DB 2; Length 149;
Best Local Similarity 28.7%; Pred. NO. 10;
Matches 27; Conservative 16; Mismatches 36; Indels 15; Gaps 4;

QY	55	YKMKSPGLGICLIID-----CIGNETELLRDT--FTSLGYEVQKFLHLSMHGISQI	103
DB	17	YEMNSNPRGTVLILSNENFKNMRRVGTQDEVNLTFLFKLQYTVICKNLEAESMLEA	76
QY	104	LQGFACMPHEDYDSFVCLVSRG-GSQSVYGV	136
DB	77	INEFA---EWAHTDSIILFLSHGAGSVFGID	107

RESULT 2

AE2322
hypothetical protein alr4132 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AE2322
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.; Nakazaki, N.; Shimo, S.; 2001
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena sp. PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE2322
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-135 <KUR>
A:Cross-references: UNIPROT:Q8YPR0; GB:BA000019; PIDN:BA075831.1; PID:gl7133367; GSPDB:GN
A:Experimental source: strain PCC 7120
C:Genetics:
C:Gene: alr4132
C:Superfamily: Escherichia coli ybdQ protein

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Query Match          7.6%; Score 70.5; DB 2; Length 135;
Best Local Similarity 33.8%; Pred. No. 17;
Matches 25; Conservative 15; Mismatches 27; Indels 7; Gaps 4;

QY 4 VQAGTSYRNVLQAAIQKSLKDPNSN---NFRPEPVKKSIOESEA-FLPQSIPEERYKMKS 59
Db 26 VQKYGS--RLILSVVEESPDSASSPMVSPVAVKLLRDAQALFLQOGIPSEIVEKQG 83
QY 60 KP-LGICIIIDCIG 72
Db 84 KPAFTICDAVEIG 97

RESULT 3
A97355
hypothetical protein CAC3708 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: A97355
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: A97355
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-152 <KUR>
A;Cross-references: UNIPROT:Q97CY2; GB:AE001437; PIDN:AAK81628.1; PID:gl5026813; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC3708

Query Match          7.4%; Score 69; DB 2; Length 152;
Best Local Similarity 28.9%; Pred. No. 28;
Matches 22; Conservative 16; Mismatches 26; Indels 12; Gaps 2;

QY 19 IQKSLKDPNSNFRPEPVKKSIOESEAFLPOSIPERYKMKSPLGLICIIDCIGNETELL 78
Db 86 LKKALDAPTASKKKEPVKEPVKIVETAMPKAEAEVKKVPKSTP-----VKKEPENP 136
QY 79 RDTFTSL--GYEVQK 91
Db 137 YDPFYKLKHGKEVKK 152

RESULT 4
T08216
outer arm dynein light chain, 19K - Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08216
R;Patel-King, R.S.; Benashski, S.E.; Harrison, A.; King, S.M.
J. Cell Biol. 137, 1081-1090, 1997
A;Title: A Chlamydomonas homolog of the putative murine t complex distorter Tctex-2 is a
A;Reference number: Z16406; MUID:97311077; PMID:9166408
A;Accession: T08216
A;Status: preliminary;
A;Molecule type: mRNA
A;Residues: 1-136 <PAT>
A;Cross-references: UNIPROT:O04355; EMBL:U089649; NID:g2138333; PID:g2138334
A;Experimental source: strain 1132D

Query Match          7.4%; Score 68.5; DB 2; Length 136;
Best Local Similarity 22.6%; Pred. No. 27;
Matches 26; Conservative 28; Mismatches 40; Indels 21; Gaps 5;

QY 6 GAGTSY-RNVLQAAIQKSLKDPNSNFRPEPVK-----KSIQSEAEFLPQSIPEERYKM-- 57
Db 28 GPNTKFERHKVAVLQKVLKRIEKQKYPDKVAQISKQLADLRKVKALGYDRYKLV 87
QY 58 -----KSKPLGICLIIDCIGNETELLRDTFTSLGYEVOKELHLSMHGISOILGOF 107

```

Query 121 - CVLVSRG 127
Db 86 GCTAISTG 93

RESULT 7
T16321
hypothetical protein F41C6.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T16321
R/Gaivel, C.
submitted to the EMBL Data Library, October 1995
A/Description: The sequence of C. elegans cosmid F41C6.
A/Reference number: Z18495
A/Accession: T16321
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-164 <GBI>
A/Cross-references: UNIPROT:Q20267; EMBL:U39745; NID:g1049470; PID:g1049471; PIDN:AAA0874
C/Genetics:
A/Gene: CESP:F41C6.2
A/Introns: 51/3; 67/1

Query Match 7.0%; Score 65.5; DB 2; Length 164;
Best Local Similarity 23.2%; Pred. No. 66;
Matches 32; Conservative 16; Mismatches 39; Indels 51; Gaps 6;

Query 61 PLGICLLI-----DCIGN-----ETELLRTFTSLGVEVKFHLISM 97
Db 7 PLRSLTIYINCDCFVNLNSYVICVDSVRKKVEPDVNMKIEKAPAGLLISIMRHLSS 66
Query 98 HGISQILGQFACMPHEHRDYSFVCVL-----VSRGGSQSVYGVQDT-----HSGLP LH 145
Db 67 VGLAQVYGRV-----EQAYKEDQVLGVAQVYEGFTQYARVDQVYVRVALDHTGSPIS 121
Query 146 HIRRMFGDSCPYLAKGP 163
Db 122 N-----WILGRP 128

RESULT 8
E47758
retrovirus-related reverse transcriptase homolog - Liriodendron chinense retrotransposon
C/Species: Liriodendron chinense
C/Date: 24-Feb-1994 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C/Accession: E47758
R/Voytas, D.F.; Cummings, M.P.; Konieczny, A.; Ausubel, F.M.; Rodermel, S.R.
Proc. Natl. Acad. Sci. U.S.A. 89, 7124-7128, 1992
A/Title: copia-like retrotransposons are ubiquitous among plants.
A/Reference number: A46200; MUID:92357784; PMID:1379734
A/Contents: clone 2
A/Accession: E47758
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-89 <VOY>
A/Cross-references: UNIPROT:Q06293; GB:M944478; NID:g439435; PIDN:AAA33403.1; PID:g168308
A/Note: sequence extracted from NCBI backbone (NCBIP:1111898)
C/Superfamily: retrovirus-related polyprotein

Query Match 6.9%; Score 64.5; DB 2; Length 89;
Best Local Similarity 26.8%; Pred. No. 39;
Matches 26; Conservative 13; Mismatches 23; Indels 35; Gaps 5;

Query 86 GYEVOKF-----LHLSMHGISQILGQFACMPHEHRDYSFVCVLVSRGGSQSVYGVQDTH 139
Db 20 GYTVQGAENKVKLRRLSYGLKQLKQW-----YKFDSP---MMSRGFSKSEY-----65
Query 140 SGLFLHRRMFMGDCSPYLAG-KPKMFFIQNYVSD 175
Db 66 -----DYCVYFETLNYEKLISVIFYDD 88

A:Molecule type: DNA
A:Residues: 1-167 <PER>
A:Cross-references: UNIPROT:Q08021; EMBL:X73368; NID:g312705; PIDN:CAA51784.1; PID:g3127

Query Match 6.8%; Score 63.5; DB 2; Length 167;
Best Local Similarity 28.8%; Pred.No.1.1e+02;
Matches 23; Conservative 17; Mismatches 25; Indels 15; Gaps 4;

Qy 4 VQGAGTSYRNVLQAIIQKSLKDPNSNNPREPVPVKKSIOESEAFLPQSIP-EER--YKMWSK 60
 :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 99 IRGGLAKKLALMAL-----DHAREOGFKCYLETTFALREALYERLGFEHISE 149

Qy 61 PLGICLIIDICIGNETELLRD 80
 |||| :| | :| | :| | :| | :| | :| | :| | :| |
Db 150 PLGCTGHVDC---EVRLMKD 166

RESULT 12
All060
probable acetyltransferase STY4812 [imported] - Salmonella enterica subsp. enterica sero
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A>Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: All060
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Conington, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: All060
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-171 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD06934.1; PID:g16505582; GSFPDB:GN00176
C:Genetics:
A:Gene: STY4812

Query Match 6.8%; Score 63.5; DB 2; Length 171;
Best Local Similarity 28.8%; Pred.No.1.1e+02;
Matches 23; Conservative 17; Mismatches 25; Indels 15; Gaps 4;

Qy 4 VQGAGTSYRNVLQAIIQKSLKDPNSNNPREPVPVKKSIOESEAFLPQSIP-EER--YKMWSK 60
 :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 103 IRGGLAKKLALMAL-----DHAREOGFKCYLETTFALREALYERLGFEHISE 153

Qy 61 PLGICLIIDICIGNETELLRD 80
 |||| :| | :| | :| | :| | :| | :| | :| | :| |
Db 154 PLGCTGHVDC---EVRLMKD 170

RESULT 13
E82053
probable fibrial assembly protein PilP VC2631 [imported] - Vibrio cholerae (strain N169
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: E82053
F:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermlolaeva, M.D.; Vanatavan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, H.
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: E82053
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-172 <HEI>
A:Cross-references: UNIPROT:Q9KNU9; GB:A8004329; GB:A8003852; NID:g9657211; PIDN:AAF9577
A:Experimental source: serogroup O1; strain N16961, biotype El Tor
C:Genetics:
A:Gene: VC2631
A:Map position: 1

```

Query Match      6.6%; Score 61.5; DB 2; Length 160;
Best Local Similarity 25.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 12; Mismatches 33; Indels 21; Gaps 2;

Qy 85 LGYEYQKFLHLSM-----HGISQILQGFACMPEHRDYDSFVGVLS----- 125
Db 61 LGLDVQVFIHRLDQSSFSIFERFAHAVADIPEIEACYSLSGGDFDTMIKRVKDKMAYQA 120

Qy 126 --RGSQSVYGVQDQTHSGPLHHIRMP 151
Db 121 FMSGKGLSLPGVITRSEFVIEHKTSE 148

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Search completed: June 20, 2005, 13:44:48
Job time : 41 secs

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OM protein - protein search, using sw model

Run on: June 20, 2005, 13:33:55 ; Search time 175 Seconds
(without alignments)
517.932 Million cell updates/sec

Title: US-10-713-208-6_COPY_76_252

Perfect score: 930

Sequence: 1 KOSVQAGTSYRNVLQAIQ.....YLAGPKMFFIQNVVSDGQ 177

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 571181

Minimum DB seq length: 0
Maximum DB seq length: 177

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_prot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	277	29.8	78	Q8MJ18	Q8mj18 macaca mula
2	144	15.5	172	Q6PVY1	Q6pvy1 bos taurus
3	94.5	10.2	104	Q9UG96	Q9ug96 homo sapien
4	78.5	8.4	131	Q9CXM4	Q9cxm4 mus musculu
5	73.5	7.9	149	Q9Y056	Q9y056 caenorhabdi
6	72	7.7	176	YM04_VIEBPA	Q87nm7 vibrio para
7	70.5	7.6	135	Q8YPER0	Q8yp0 anabaena sp
8	69	7.4	152	Q97CY2	Q97cy2 clostridium
9	68.5	7.4	136	Q04355	O04355 chlamydomon
10	68.5	7.4	159	Q6F7W6	Q6f7w6 acinetobact
11	68	7.3	89	Q93J15	Q93j15 streptomyc
12	68	7.3	137	LYC_BOMMO	P48816 bombyx mori
13	67.5	7.3	174	Q734A9	Q734a9 bacillus ce
14	67	7.2	125	Q669Y8	Q669y8 yersinia ps
15	67	7.2	125	Q8ZDW3	Q8zdw3 yersinia pe
16	66	7.1	96	Q9AXB5	Q9axb5 oryza sativ
17	66	7.1	133	Q7P252	Q7p252 chromobacte
18	65.5	7.0	145	Q6ZZX9	Q6zzx9 platichthys
19	65.5	7.0	164	Q202X9	Q202x9 caenorhabdi
20	64.5	6.9	89	Q06293	Q06293 liroidendro
21	64.5	6.9	114	Q98478	Q98478 paramelic
22	64.5	6.9	125	Q9DDM5	Q9ddm5 corytophane
23	64.5	6.9	135	Q9B581	Q9b581 lacerta viv
24	64.5	6.9	150	Q7SXI3	Q7sxi3 brachydanio
25	64.5	6.9	174	1 RIMW_TREPA	Q83877 treponema p
26	64	6.9	101	VE7_HPV21	P50779 human papil
27	64	6.9	119	Q9P816	Q9p816 issatchenki
28	64	6.9	135	Q9B579	Q9b579 lacerta viv
29	64	6.9	151	DKSA_BUCAP	Q8k9us buchnera ap
30	63.5	6.8	135	Q9B0R7	Q9b0r7 lacerta viv
31	63.5	6.8	135	Q9B0R8	Q9b0r8 lacerta viv

32	63.5	6.8	135	2	Q9B580	Q9b580 lacerta viv
33	63.5	6.8	135	2	Q9B583	Q9b583 lacerta viv
34	63.5	6.8	135	2	Q9B586	Q9b586 lacerta viv
35	63.5	6.8	153	2	Q994A0	Q894a0 clostridium
36	63.5	6.8	167	1	YJGM_SALTY	Q802i1 salmonella
37	63.5	6.8	171	2	Q821Z0	Q821z0 salmonella
38	63	6.8	132	2	Q6DNH3	Q6dnh3 uncultured
39	63	6.8	172	2	Q9KNU9	Q9knu9 vibrio chol
40	62.5	6.7	110	2	Q84SM2	Q84sm2 oryza sativ
41	62.5	6.7	119	2	Q6FVN0	Q6fvn0 candida gla
42	62.5	6.7	126	2	Q9NGQ9	Q9ngq9 tribolium c
43	62.5	6.7	127	2	Q79F17	Q79f17 enterococc
44	62.5	6.7	135	2	Q8LU47	Q8lu47 zootoca viv
45	62.5	6.7	135	2	Q9B1W8	Q9b1w8 lacerta viv

ALIGNMENTS

RESULT 1

Q8MJ18 PRELIMINARY; PRT; 78 AA.
AC Q8MJ18;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Fllice/caspase-1 inhibitory protein (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Petit F., Arnould D., Lelievre J.-D., Lecossier D., Hance A.J.,
RA Monceaux V., Ho Tsong Fang R., Hurtrel B., Ameisen J.-C.,
RA Estaquier J.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF530077; AAC95637.1;
FT NON_TER 1
FT NON_TER 78
SQ SEQUENCE 78 AA; 8971 MW; 6BD208095731A99 CRC64;

Query Match 29.8%; Score 277; DB 2; Length 78;
Best Local Similarity 73.1%; Pred. No. 6.4e-19;
Matches 57; Conservative 2; Mismatches 1; Indels 18; Gaps 1;

QY 11 YRNVLQAAATSKSLKDPSSNNFR-----EPPVKKSIOESEAFLPOSIE 52
Db 1 YKNVLQAAATQSLKDPSSNNFRLLHNGRSKQRLKEQLGTQOEPVKTSIQESEAFLPOSIE 60
QY 53 ERYKMKSKPLGICLIIDC 70
Db 61 ERYKMKSKPLGICLIIDC 78

RESULT 2

Q6PVY1 PRELIMINARY; PRT; 172 AA.
AC Q6PVY1;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Caspase-3 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Tao W., Mallard B., Karrow N., Bridle B.;
RT "Construction and application of a bovine immune-endocrine cDNA

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RT microarray.";
RL Vet. Immunol. Immunopathol. 101:1-17(2004).
CC -!- SIMILARITY: Belongs to the peptidase C14 family.
DR EMBL; AY575000; AAS93968.1; -.
DR HSSP; P55210; 1K86.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolase; Protease; Thiol protease; Zymogen.
FT NON_TER 1
FT NON_TER 172
FT NON_TER 172
SQ SEQUENCE 172 AA; 19333 MW; 6CEB4E7920693A9D CRC64;

Query Match 15.5%; Score 144; DB 2; Length 172;
Best Local Similarity 31.1%; Pred. NO. 1e-05;
Matches 38; Conservative 24; Mismatches 42; Indels 18; Gaps 5;

QY 62 LGICLIID-----C-IGNETEL--LRDTFTSLGYEQKFLHLSMGISQILGQF 107
DB 3 MGLCIILNNKFNHENTGMARSGTGDVAANLRFTFMNLYEVRKNDLTCKEMLELMSNV 62

QY 108 ACMPHERDYDSFVCVLVSRGGSSVGVQDTHSGGLPLHHIRRMFMGDCSPYLAKPKMPFF 167
DB 63 S-KEDHSKSSPICVLLSHGEGILFG---TNGPVNKKLASFFRGDYCRSLTGPKLFI 118

QY 168 IQ 169
DB 119 IQ 120

RESULT 3
Q9UG96 PRELIMINARY; PRT; 104 AA.
AC Q9UG96;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp586A181 (Fragment).
GN Name=DKFZp586A181;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
RA Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050391; CAB43686.2; -.
DR HSSP; P29466; 1ICE.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 104 AA; 11587 MW; 10411DF1306C1432 CRC64;
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Query Match 10.2%; Score 94.5; DB 2; Length 104;
Best Local Similarity 28.4%; Pred. NO. 0.33;
Matches 27; Conservative 18; Mismatches 47; Indels 3; Gaps 2;

QY 78 LRDTFTSLGYEQKFLHLSMGISQILGQFACMPHERDYDSFVCVLVSRGGSSQSVGV-- 135
DB 3 MKELLEGDYSDVVEENLTARDMESALRAFATRPHEKSSDSTFLVMSHGILGICGTVH 62

QY 136 DQTHSGGLPLHH-IRRMFMGDCSPYLAKPKMPFFIQ 169
DB 63 DEKPDVLLYDTIFQIFNNRNCLSLKDKPKVLIIVQ 97

RESULT 4
Q9CKM4 PRELIMINARY; PRT; 131 AA.
ID Q9CKM4
AC Q9CKM4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched
DE library, clone:3110059017 product:caspase 3, apoptosis related
DE cysteine protease, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA The FANTOM Consortium;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara S., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
```

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Hanakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kaya S., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koyasu T., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito K., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK014231; BAB29219.1; -.
DR HSSP; P42574; INME.
DR GO; GO:0030693; F:caspace activity; IEA.
DR GO; GO:008233; F:peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR PRINTS; PR00376; ILIBENZYME.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Peptidase.
SQ SEQUENCE 131 AA; 14799 MW; 2B36D12AC47F62C7 CRC64;

Query Match 8.4%; Score 78.5; DB 2; Length 131;
Best Local Similarity 27.5%; Pred. No. 15;
Matches 30; Conservative 19; Mismatches 37; Indels 23; Gaps 6;

QY 28 NNFREPPV--KKSIOSEAFLOSIPEERYKMSKPLGICLIID-----CIGN 73
Db 14 NNFVKTIGSKSV-DSGIYLDSS-----YKMDYPEMGICIIINNKNFKHSTMSRSRG 67

QY 74 ETEL--LRDTFTSLGYEVQKFLHSMHGISQILGQFACMP-EHRDYDSF 119
Db 68 DVDAAANLRETFMGLKQVRKNKNDLTREDILELMDSGKIEPIQSRGSGF 116

RESULT 5
QY056 PRELIMINARY; PRT; 149 AA.
AC QY056;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Caspase-related protein 1C (Hypothetical protein Y48E1B.13c).
GN Name=csp-1; Synonyms=Y48E1B.13c; ORFNames=Y48E1B.13;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2;
RX MEDLINE=99074291; PubMed=9857046; DOI=10.1074/jbc.273.52.35109;
RA Shaham S.;
RT "Identification of multiple Caenorhabditis elegans caspases and their
RT identical roles in proteolytic cascades.";
RL J. Biol. Chem. 273.35109-35117 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology.";
RL Science 282.2012-2018 (1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA McMurray A.A.;
FT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF088287; AAC98294.1; -.
DR EMBL; Z93393; CAD18880.1; -.
DR FIR; T43637; T43637.
DR HSSP; P42575; LPYO.
DR WormBase; WBGene00000819; csp-1.
DR WormPep; Y48E1B.13c; CE30017.
DR GO; GO:0030693; F:caspace activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR PRINTS; PR00376; ILIBENZYME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hypothetical protein.
SQ SEQUENCE 149 AA; 16921 MW; 0C5943D53DE16BC7 CRC64;

Query Match 7.9%; Score 73.5; DB 2; Length 149;
Best Local Similarity 28.7%; Pred. No. 53;
Matches 27; Conservative 16; Mismatches 36; Indels 15; Gaps 4;

QY 55 YKMKSKPLGICLIID-----CIGNETELLRDT--FTSLGYEVQKFLHLSMHGISQI 103
Db 17 YEMNSNPRGTVLILSNENFKMERRVGTQKDEVNLTKLQKLYTVICKRNLEAESMLEA 76

QY 104 LQQFACMPEHRDYDSFVCLVSRG-GSQSVYGVGD 136
Db 77 IKEFA---EMAHTDSIIILFLLSHGDGAGSVFGID 107

RESULT 6
YMO4_VIBPA STANDARD; PRT; 176 AA.
AC Q87MM7;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical UPF0115 protein VP2204.
GN OrderedLocNames=VP2204;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361.743-749 (2003).
CC -!- SIMILARITY: Belongs to the UPF0115 family.
CC -!- SIMILARITY: Contains 1 Smr domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AP005080; BAC60467.1; -.
DR HAMAP; MF_01042; -.
DR InterPro; IPR002625; Smr/MutS2_C.
DR Pfam; PF01713; Smr; 1.
DR SMART; SM00463; SMR; 1.
DR PROSITE; PS50828; SMR; 1.
KW Complete proteome; Hypothetical protein.
FT DOMAIN 97 172 Smr
SQ SEQUENCE 176 AA; 20200 MW; D6562D0E7D7EDC46 CRC64;
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Query Match          7.7%; Score 72; DB 1; Length 176;
Best Local Similarity 23.9%; Pred. No. 90;
Matches 37; Conservative 31; Mismatches 53; Indels 34; Gaps 9;

QY 1 KOSVQAGTSYRNVLQAAIKSLKDPNNFREPEVKSIQSEAFPLQSIPE 52
DB 16 KEAVQGV-----KKLRQDTI---IQPKNTKQKEIKSRNREASDSEFYFSDFVPLNBE 68
QY 53 -----ERYKMSKPLGIC---LIIDCIG-NETELLRTFTSLGVEVKFHLHS-- 96
DB 69 GTRYARDVSYEVRKLRGVYDPVFLDMGMTQOEAKRELGAIAVCVKNRHCACV 128
QY 97 MHGISQ-ILGQFA--CMPEHRDYDSVVCVLVRGG 128
DB 129 QHGIGHILKQAPLQAHPDWMFHPQAPLEFGG 163

RESULT 7
Q8YPRO PRELIMINARY; PRT; 135 AA.
AC Q8YPRO;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alr4132 protein.
GN OrderedLocusNames=alr4132;
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Rep. 8:205-213(2001).
DR EMBL; AF003595; BAB75831.1; -.
DR PIR; AE2322; AE2322.
DR HSSP; Q57997; 1MJH.
DR GO; GO:0006950; P:response to stress; IEA.
DR Pfam; PF00582; Usp; 1.
DR PRINTS; PR01439; UNVRSLSSTRESS.
KW Complete proteome.
SQ SEQUENCE 135 AA; 1442 MW; BF77512CB6FA6BC2 CRC64;

Query Match          7.6%; Score 70.5; DB 2; Length 135;
Best Local Similarity 33.8%; Pred. No. 91;
Matches 25; Conservative 15; Mismatches 27; Indels 7; Gaps 4;

QY 4 VQAGTSYRNVLQAAIKSLKDPNN---NFREPEVKSIQSEAFPLQSIPEERYKMS 59
DB 26 VQKYGSG--RLILSVVESSPDSSADPMWSPFAVKLLRDAQALFLOQGISPIVEKQG 83
QY 60 KP-LGICLIIDCIG 72
DB 84 KPAFTICDVADEIG 97

RESULT 8
Q97CY2 PRELIMINARY; PRT; 152 AA.
AC Q97CY2;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein CAC3708.
GN OrderedLocusNames=CAC3708;
OS Clostridium acetobutylicum.

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VOM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RX DOI=10.1128/JB.183.16.4823-4838.2001;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Oiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,
RA Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AE007866; AAK81628.1; -.
DR PIR; A97355; A97355.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 152 AA; 17127 MW; 24EB2335E1D66FED CRC64;

Query Match          7.4%; Score 69; DB 2; Length 152;
Best Local Similarity 28.9%; Pred. No. 1.5e+02;
Matches 22; Conservative 16; Mismatches 26; Indels 12; Gaps 2;

QY 19 IQKSLKDPNNFREPEVKSIQSEAFPLQSIPEERYKMSKPLGICLIIDCIGNETELL 78
DB 86 LKKALDAPTASKKEPVKPKIVETAMPKAEAEVKVPKSTP-----VKKEPENP 136
QY 79 RDTFTSL---GYEQVK 91
DB 137 YDPFYKLRKHGKEVKK 152

RESULT 9
O04355 PRELIMINARY; PRT; 136 AA.
ID O04355
AC O04355;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mr19,000 outer arm dynein light chain.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1132D;
RX MEDLINE=97311077; PubMed=9166408; DOI=10.1083/jcb.137.5.1081;
RA Patel-King R.S., Benashski S.E., Harrison A., King S.M.;
RT "A Chlamydomonas homologue of the putative murine t complex distorter
RT Tctex-2 is an outer arm dynein light chain.";
RL J. Cell Biol. 137:1081-1090(1997).
DR EMBL; U89649; AAB58383.1; -.
DR PIR; T08216; T08216.
DR InterPro; IPR005334; Tctex.
DR Pfam; PF03645; Tctex-1; 1.
DR SEQUENCE 136 AA; 15883 MW; A42D37012E91262A CRC64;

Query Match          7.4%; Score 68.5; DB 2; Length 136;
Best Local Similarity 22.6%; Pred. No. 1.4e+02;
Matches 26; Conservative 28; Mismatches 40; Indels 21; Gaps 5;

QY 6 GAGTSY-RNVLQAAIKSLKDPNNFREPEVK-----KSIQSEAFPLQSIPEERYK-- 57
DB 28 GNTKFERHKVQAVLKQVLKRIEKQKYDPVKGAQISQLADDLREKVALGYDKYKVI 87
QY 58 -----KSKPLGICLIIDCIGNETELLRTFTSLGVEVKFHLHSMHGISQILGQF 107
DB 88 QVTGQKQGMRIISRLCLWDQT---NDNFASEYENE-----SMYCVQVVGLY 134

RESULT 10
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Q6F7W6 PRELIMINARY; PRT; 159 AA.

AC Q6F7W6; 159 AA; Score 68.5; DB 2; Length 159; Best Local Similarity 20.9%; Pred. No. 1.7e+02; Matches 28; Conservative 23; Mismatches 30; Indels 53; Gaps 7;

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Hypothetical protein.

DE OrderedLocusNames=AC12AD3160;

GN Acinetobacter sp. (strain ADP1).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Moraxellaceae; Acinetobacter.

OX NCBI_TaxID=62977;

RN [1]

RP SEQUENCE FROM N.A.

RA Barbe V., Vallenet D., Fonknechten N., Kreimeyer A., Oztas S., Labarre L., Cruveiller S., Robert C., Duprat S., Wincker P., Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.; "Unique features revealed by the genome sequence of Acinetobacter sp. ADP1, a versatile and naturally transformation competent bacterium."; RL Nucleic Acids Res. 0:0-0(2004).

DR EMBL: CR543861; CAG69849.1; --.

DR InterPro: IPR020336; UPF0054.

DR Pfam: PF02130; UPF0054; 1.

DR ProDom: PD005688; UPF0054; 1.

DR TIGRFAMs: TIGR00043; UPF0054; 1.

DR PROSITE: PS01306; UPF0054; 1.

KW Complete proteome.

SQ SEQUENCE 159 AA; 17922 MW; ECCA1638997EE06D CRC64;

Query Match 7.4%; Score 68.5; DB 2; Length 159; Best Local Similarity 20.9%; Pred. No. 1.7e+02; Matches 28; Conservative 23; Mismatches 30; Indels 53; Gaps 7;

QY 15 LQAIIQKSLKPSNNPREPVKSIQ-----ESEAFL----- 46

DB 3 LNLSLQAQFKSPDLAKRAHKAIETLHDHVEKTDSEIGIACVDHQSHRLNLEYRCK 62

QY 47 -----POSIPERYK-MKSKPLG---ICL--IIDICIGNETELLRTFTSLGVEYCK 91

DB 63 DKSTNVLSFSPDIPESVLPDLDPGLDVCIPVVLD-----EAIEQHKTAQAH---- 112

QY 92 FLHLSMHGHSQILG 105

DB 113 FHHMLVHGTLHLG 126

QY 93J15 PRELIMINARY; PRT; 89 AA.

AC Q93J15; 89 AA; Score 68.5; DB 2; Length 89; Best Local Similarity 20.9%; Pred. No. 1.7e+02; Matches 28; Conservative 23; Mismatches 30; Indels 53; Gaps 7;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-WAR-2003 (TREMBLrel. 23, Last annotation update)

DE Hypothetical protein SC03993.

GN ORFNames=SCBAC25E3.30c;

OS Streptomyces coelicolor.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycineae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1902;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2) / M145;

RC MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;

RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S., Rabinowitch E., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Saunders D., Sharp S., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J., Hopwood D.A.; "Complete genome sequence of the model actinomycete Streptomyces

RT "Complete genome sequence of the model actinomycete Streptomyces

RT coelicolor A3(2)";

RL Nature 417:141-147(2002).

DR EMBL: AL939118; CAC44717.1; --.

KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 89 AA; 10063 MW; 02FB9B00B1068C2 CRC64;

Query Match 7.3%; Score 68; DB 2; Length 89; Best Local Similarity 33.3%; Pred. No. 96; Matches 21; Conservative 11; Mismatches 17; Indels 14; Gaps 4;

QY 108 ACPMP-----EHRDYSFVCLVSRGQS-QS-VYGVDTQTHSGLPLHH-----IRMFMDGSCP 157

DB 26 ACLTSEYVSHRDAIFVNCU-----GPRQSRHYVYVNETHEGCPVIHSARWPDVDMFVGNACC 81

QY 158 YLA 160

DB 82 VVA 84

RESULT 12

LVC_BOMMO STANDARD; PRT; 137 AA.

ID LVC_BOMMO

AC P48816; Q9TWL7;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Lysozyme precursor (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase).

OS Bombyx mori (Silk moth).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;

OC Bombycidae; Bombyx.

OX NCBI_TaxID=7091;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Fat body;

RC MEDLINE=95394356; PubMed=7665079; DOI=10.1016/0378-1119(95)00199-G;

RA Lee W.J., Brey P.T.; "Isolation and characterization of the lysozyme-encoding gene from the silkworm Bombyx mori."; RL Gene 161:199-203(1995).

RN [2]

RP SEQUENCE OF 19-38, AND FUNCTION.

RC STRAIN=NB19; TISSUE=Larval hemolymph;

RC MEDLINE=95181849; PubMed=7876591; DOI=10.1006/jipa.1995.1003;

RA Abraham E.G., Nagaraju J., Salunke D., Gupta H.M., Datta R.K.; "Purification and partial characterization of an induced antibacterial protein in the silkworm, Bombyx mori."; RL J. Invertebr. Pathol. 65:17-24(1995).

CC -!- FUNCTION: Lysozymes have primarily a bacteriolytic function; those in tissues and body fluids are associated with the monocyte-macrophage system and enhance the activity of immunogens. Active against E.coli and M.luteus.

CC -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between N-acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan heteropolymers of the prokaryotes cell walls.

CC -!- DEVELOPMENTAL STAGE: Expressed within 6 hours after induction, reaches maximum levels after 48 hours and declines after 72 hours after induction.

CC -!- INDUCTION: By bacterial infection.

CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 22 family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL: L37416; AAB40947.1; --.

DR PIR: JC4233; JC4233.

DR PDB: 1GD6; X-ray; A=19-137.

DR InterPro: IPR001916; Glyco_hydro_22.

```
DR InterPro; IPR000974; Glyco_hydro_22Ly.
DR Pfam; PF00062; Lys; 1.
DR PRINTS; PR00137; LYSOZYME.
DR PROSITE; PS00128; LACTALBUMIN_LYSOZYME; 1.
DR SMART; SM00263; LYZ1; 1.
DR 3D-structure; Antibiotic; Bacteriolytic enzyme;
KW Direct protein sequencing; Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 18
FT CHAIN 19 137
FT DISULFID 24 137
FT DISULFID 45 127
FT DISULFID 79 93
FT DISULFID 89 107
FT ACT_SITE 50 50
FT ACT_SITE 67 67
FT STRAND 20 20
FT HELIX 23 32
FT TURN 33 34
FT HELIX 37 39
FT HELIX 40 50
FT TURN 51 53
FT STRAND 54 54
FT TURN 55 56
FT STRAND 58 60
FT TURN 62 63
FT STRAND 66 68
FT TURN 69 72
FT STRAND 73 74
FT TURN 75 78
FT STRAND 80 80
FT STRAND 86 86
FT TURN 87 90
FT STRAND 91 92
FT HELIX 93 96
FT HELIX 102 115
FT HELIX 116 119
FT HELIX 121 124
FT TURN 125 126
FT TURN 135 137
SQ SEQUENCE 137 AA; 15668 MW; FFE5710506C61A1D CRC64;

Query Match 7.3%; Score 68; DB 1; Length 137;
Best Local Similarity 28.0%; Pred. No. 1.6e+02;
Matches 21; Conservative 16; Mismatches 24; Indels 14; Gaps 5;

QY 66 LIIDICIGNETELLRTFTSLG--YEVQKFLHLSMHGISO-ILGQFACMPPEHRDYSFVCV 122
Db 9 LVVLCVGSSEAK----TFTRCGLVHELK-----HGFEENLMRNWVCLVEHESSRDTSKT 58
QY 123 LVSRGSGSQSVYGVQDQ 137
Db 59 NTRNGSKD-YGLFQ 72

RESULT 13
Q734A9 PRELIMINARY; PRT; 174 AA.
AC Q734A9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Acetyltransferase. GNAT family.
GN OrderedLocusNames=BCE3498;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=222523;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Heigason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;

RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXO1.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017275; AAS42404.1; -.
DR TIGR; BCE3498; -.
DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR InterPro; IPR000182; GCM5acetyl trans.
DR Pfam; PF00583; Acetyltransf 1; 1.
KW Complete proteome; Transferase.
SQ SEQUENCE 174 AA; 19314 MW; 13539D8DED4B6945 CRC64;

Query Match 7.3%; Score 67.5; DB 2; Length 174;
Best Local Similarity 21.5%; Pred. No. 2.4e+02;
Matches 37; Conservative 28; Mismatches 56; Indels 51; Gaps 7;

QY 9 TSYRNVLOAAIQKSLKDPSPNNFREPPVKKSIOSEAEFLPQ----SIPEE--RYKMKSKPL 62
Db 10 TDYRKTEEVVQQAFLNEEFSDKKEHLVKRIRECDAFPELSIVAVDEIYGHIMLSK-- 67
QY 63 GICLIIDICIGNETELLRTFTSLGYE-----VQKFLHLSMHGISOILGQFACM 110
Db 68 -ITIEQDQASVDSLALAPVSVARGYQKKGIGKLIIVAALEKAKELG-YGSVVVLG----- 120
QY 111 PEHRDY-----DSFVCVLVSRGSGSQSVYGVQDQTHS 140
Db 121 --HSEYVPKFGFKKASEWNKAPPEVDPDEAFMAVELSENALQGIIEGVVQYSS 170

RESULT 14
Q669Y8 PRELIMINARY; PRT; 125 AA.
AC Q669Y8;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE Putative membrane protein.
GN ORFNames=YPTB2344;
OS Versinia pseudotuberculosis IP 32953.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Versinia.
OX NCBI_TaxID=273123;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP 32953;
EX PubMed=15358858;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V.,
RA Brubaker R.R., Fowler J., Hinnebusch B.J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RA "Insights into the genome evolution of Versinia pestis through whole
RT genome comparison with Versinia pseudotuberculosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
DR EMBL; BX936398; CAH21582.1; -.
SQ SEQUENCE 125 AA; 14120 MW; 0509AC4B2D1A3885 CRC64;

Query Match 7.2%; Score 67; DB 2; Length 125;
Best Local Similarity 25.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 10; Mismatches 15; Indels 26; Gaps 2;

QY 86 GYEVQKFLHLSMHGISOILGQFACMPE-----HRDYDSFV----- 120
Db 26 GYQLAKFIRVVMHSHGQAIDKKKCLPRTPDPVHRVYISFVNHNHSAKNDLHYRLLLSSA 85
QY 121 -CVLVSRG 127
Db 86 GCIAISTG 93

RESULT 15
Q82DW3 PRELIMINARY; PRT; 125 AA.
ID Q82DW3
```

Search completed: June 20, 2005, 13:44:04
Job time : 177 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 13:30:56 ; Search time 160 Seconds
(without alignments)

427.854 Million cell updates/sec

Title: US-10-713-208-6_COPY_76_252

Perfect score: 930

Sequence: 1 KQSVQAGTSYRNVLQAAIQ.....YLAGKPKMFQIYVVSQDQ 177

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1389662

Minimum DB seq length: 0
Maximum DB seq length: 177

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	325	34.9	175	2	AAY05794 MRIT-D/S
2	166	17.8	147	7	ADL18190 Human cas
3	166	17.8	147	8	ADP20044 Human cas
4	154	16.6	167	4	AAM31155 Peptide #
5	130	14.0	163	4	AAM68529 Human bon
6	130	14.0	163	5	ABG38107 Human pep
7	108	11.6	158	5	AAE16024 Human cas
8	102	11.0	125	4	AAO2627 Human pol
9	78	8.4	146	8	ADO63844 Human 213
10	73	7.8	39	3	AB14254 Partial m
11	71.5	7.7	101	6	ADA41128 Human sec
12	71.5	7.7	101	6	ABR47936 Human sec
13	71.5	7.7	101	6	ABR00176 Human gen
14	71.5	7.7	101	7	ADB91676 Human sec
15	71.5	7.7	101	7	ADC74344 Human sec
16	71.5	7.7	102	2	AAY41346 Human sec
17	70.5	7.6	173	8	ADL05651 M. catarr
18	67.5	7.3	133	6	ADB07674 Alloiococ
19	66.5	7.2	102	5	ABP31818 Human ORF
20	66.5	7.2	169	5	ABU51964 Helicobac
21	66	7.1	167	8	ADO3472 B. subtil
22	65	7.0	100	6	ABP60619 Human zin
23	65	7.0	117	2	AAY12157 Human 5'
24	64.5	6.9	174	6	ABU48709 Protein e
25	64	6.9	130	6	ABM5939 Propionib

ALIGNMENTS

RESULT 1

AAY05794

ID AAY05794 standard; protein; 175 AA.

XX AAY05794;

XX AAY05794;

DT 02-AUG-1999 (first entry)

XX AAY05794;

DE MRIT-D/S polypeptide.

XX AAY05794;

KW MRIT-D/S; MACH related inducer of toxicity; human; apoptosis;

KW anti-apoptotic; cancer; autoimmune disease; angiogenesis;

KW atherosclerosis; neurodegenerative disease; Alzheimer's disease;

KW Parkinson's disease; retinitis pigmentosa; stroke; AIDS; infection;

KW aplastic anaemia; myocardial infarction; therapy; mutant.

XX Homo sapiens.

OS Synthetic.

XX AAY05794;

PN WO9918230-A2.

XX AAY05794;

PD 15-APR-1999.

XX AAY05794;

PF 07-OCT-1998; 98WO-US021132.

XX AAY05794;

PR 07-OCT-1997; 97US-00946226.

XX AAY05794;

PA (UNIW) UNIV WASHINGTON.

XX AAY05794;

PI Chaudhary PM;

XX AAY05794;

DR WPI; 1999-277275/23.

XX AAY05794;

PT Identifying regulators of MACH-related inducer of toxicity.

XX AAY05794;

PS Example 2; Page; 78pp; English.

XX AAY05794;

CC The present sequence represents MRIT-D/S, comprising amino acid residues

CC 306-480 of novel human MACH-related inducer of toxicity MRIT alpha 1 (see

CC AAY05787). This deletion mutant was used to examine the interaction of

CC MRIT alpha 1 with caspases. The FLICE-p20 domain interacted with MRIT

CC alpha 1 but not with MRIT-D/S. The invention provides multiple isoforms

CC of MRIT (see AAY05787-89), isolated active fragments of which have either

CC pro-apoptotic or anti-apoptotic activity. Selective enhancers and

CC inhibitors of MRIT apoptotic activity can be identified and used to treat

CC diseases mediated by the dysfunction of programmed cell death or

CC proliferation, such as cancer or a neurodegenerative disorder. Note: the

CC present sequence is not shown in the specification but is derived from

Aau65771 Propionib
Abm62290 Propionib
Abu45215 Protein e
Abu48266 Protein e
Adb07666 Alloiococ
Adb07668 Alloiococ
Aae22127 Human 543
Aab80170 Corynebacc
Abj26430 Aspergill
Adk48469 Streptoco
Aay35470 Chlamydia
Ada33022 Acinetoba
Aab53691 Lactococc
Aay85882 S. pneumo
Aae35761 Human SEC
Abp69784 Human pol
Aau27633 Human pro
Ads06637 Staphyloc
Aam35040 Peptide #
Abb27326 Protein #

26 64 6.9 139 4 AAU65771
27 64 6.9 139 6 ABM62290
28 63.5 6.8 166 6 ABU45215
29 63.5 6.8 171 6 ABU48266
30 63 6.8 113 6 ADB07666
31 63 6.8 134 6 ADB07668
32 63 6.8 153 5 AAE22127
33 62.5 6.7 138 4 AAB80170
34 62.5 6.7 167 6 ABJ26430
35 62.5 6.7 177 8 ADK48469
36 62 6.7 140 2 AAY35470
37 62 6.7 161 6 ADA33022
38 61.5 6.6 156 5 AAB53691
39 61 6.6 134 2 AAY85882
40 61 6.6 142 6 AAE35761
41 61 6.6 159 5 ABP69784
42 60.5 6.5 149 4 AAU27633
43 60.5 6.5 160 8 ADS06637
44 60 6.5 109 4 AAM35040
45 60 6.5 109 4 ABB27326

CC the MRIT alpha 1 sequence given in figure 1F
XX Sequence 175 AA;
SQ

Query Match 34.9%; Score 325; DB 2; Length 175;
Best Local Similarity 98.4%; Pred. No. 2.5e-30;
Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 117 DSFVCLVSRGGSQSVYGVDOHSGPLPLHHRMFWDSCPYLAGKPKMFFIQNVVSDG 176
DB 1 DSFVCLVSRGGSQSVYGVDOHSGPLPLHHRMFWDSCPYLAGKPKMFFIQNVVSEG 60

QY 177 Q 177
DB 61 Q 61

RESULT 2
ID ADL18190
AC ADL18190;
XX
XX 06-MAY-2004 (first entry)
DT Human caspase 3 large subunit SEQ ID NO:110.
DE
XX chimeric protein; signal protein; trafficking signal targeting;
KW proteolytic cleavage site; protease; protease inhibitor; enzyme; human;
KW caspase 3.
XX Homo sapiens.
OS
XX WO2003014381-A1.
PN
XX 20-FEB-2003.
PD
XX
XX 08-AUG-2002; 2002WO-KR001515.
PF
XX
XX 10-AUG-2001; 2001KR-00048123.
PR
XX (AHRA-) AHRAM BIOSYSTEMS INC.
PA
XX Hwang I, Kim DH, Lee YJ;
PI WPI; 2003-256596/25.
XX N-PSDB; ADL18189.
DR
XX New chimeric protein, useful for detecting protease inhibitors inside the
PT cell or tissue.
PT
XX Disclosure; SEQ ID NO 110; 214pp; English.

The present invention describes a chimeric protein comprising at least one signal protein that has a trafficking signal targeting to a subcellular organelle and at least one proteolytic cleavage site for a protease. The chimeric protein is constructed, so that: (a) the trafficking signals of all the signal proteins are inactivated by linking the proteolytic site or a signal masking protein through the proteolytic site to the N- or C- terminus of the signal proteins, and so the chimeric protein is present in cytosol; (b) the trafficking signal of at least one signal protein is activated when the proteolytic cleavage site is cleaved by the protease, and as a result at least one fragment protein that includes the activated signal protein is transported to a subcellular organelle; and (c) the chimeric protein is labelled with at least one fluorescent protein and the position and intensity distribution of the fluorescent label signal in the cell is altered depending on the cleavage by the protease. Also described: (1) a recombinant gene comprising a nucleic acid sequence encoding the chimeric protein which is constructed to express the chimeric protein in a cell; (2) a cell transformed with the recombinant gene or vector; (3) analysing the activity of a protease in vivo; (4) screening protease inhibitors in vivo; (5) a system for detecting a protease inside a cell; (6) a nucleic acid comprising the

CC sequence encoding the chimeric protein for detecting protease activity in a cell; (7) a vector comprising the nucleic acid; (8) a kit for detecting a protease inside a cell comprising the chimeric protein or the vector; (9) detecting a protease inside a cell or tissue; and (10) detecting a protease inhibitor in vivo. The chimeric protein is useful for detecting protease inhibitors inside the cell or tissue. The present sequence represents a human caspase 3 large subunit, which is used in the exemplification of the present invention.

XX
SQ Sequence 147 AA;

Query Match 17.8%; Score 166; DB 7; Length 147;
Best Local Similarity 32.6%; Pred. No. 3e-11;
Matches 43; Conservative 22; Mismatches 49; Indels 18; Gaps 4;

QY 52 EERYKMKSKPLGICLIID-----CIGNETEL--LRDTFTSGYGVQKFLHLSM 97
DB 6 DNSYKMDYPENGLCIIINNNKFNHKSTGMTSSRGTDVAANLRETFRNLYKEVYRNKNDLTR 65
QY 98 HGISQILGQFACMPHEHRDYSFVCLVSRGGSQSVYGVDOHSGPLPLHHRMFWDSCPY 157
DB 66 EEIVELMRDVS-KEDHKSRSFVCLVLSHGEGIFG---TNGPVDLKKITNPFGRDCR 121
QY 158 YLAGKPKMFFIQ 169
DB 122 SLTGKPKLFIQ 133

RESULT 3
ADP20044
ID ADP20044 standard; protein; 147 AA.
XX
XX ADP20044;
AC
XX 09-SEP-2004 (first entry)
DT
XX Human caspase-3 mature protein SEQ ID NO:9.
DE
XX human; caspase-3; stem cell differentiation; muscular dystrophy;
KW cardiovascular disease; stroke; heart failure; myocardial infarction;
KW neurodegenerative disease; neurodegenerative disorder;
KW degenerative liver disease; diabetes.
XX
XX Homo sapiens.
OS
XX WO2004053144-A2.
PN
XX 24-JUN-2004.
PD
XX 10-DEC-2003; 2003WO-CA001911.
PF
XX 10-DEC-2002; 2002US-0431990P.
PR 10-DEC-2002; 2002US-0431991P.
XX (OTTA-) OTTAWA HEALTH RES INST.
PA
XX Megeney L;
PI
XX WPI; 2004-468978/44.
DR
XX Screening for compounds that modulate stem cell differentiation comprises identifying a modulator of caspase-3 activity by contacting a caspase-3 protein, or a cell expressing a caspase-3 protein, with a candidate compound.
PT
XX Disclosure; SEQ ID NO 9; 108pp; English.

The invention relates to a novel method for screening for compounds that modulate stem cell differentiation comprising identifying a modulator of caspase-3 activity by contacting a caspase-3 protein, or a cell expressing a caspase-3 protein, with a candidate compound, measuring the activity of the caspase-3 protein and comparing the measured activity with the activity of caspase-3 protein in the absence of the candidate

Query Match 16.6%; Score 154; DB 4; Length 167;
Best Local Similarity 35.4%; Pred. No. 1e-09;
Matches 35; Conservative 18; Mismatches 38; Indels 8; Gaps 3;

QY	TRDIFSTGJELVQATLHLSNNHLSLSLQQAFCNFKRRLDSTVGVVSRKQSSQSVLHDD
db	2 LTTTFEELHFEIKPHDDCTVEQIVEILKIYQLM-DHSNMDCFCCILSHGDKGIITYGTDDGG

```

DD      2  LIIIFSEEFNFNFDDCCIVBGLIELLALIQM--DRSNMUDCFCCCLDSRSGZSLIILGILGILG
Qy      138  THSGLPLHIRRMFEMGDCSPYLAKPKPMFFIQ-----NY 171
Db      61  ORA--RIVELTSQFTGLKCPKSLAGPKVFVFIQACQGDNY 97

```

01 YEAR--PT1E1S0F10URCF8LH8GNFVFF1QACQ3DUN1 37

RESULT 3
AAM68529
ID AAM68529 standard: protein: 163 AA.

XX
AC
AAM68529;
XX

DI	06-NOV-2001	(first entry)
XX		
DE	Human bone marrow	expressed probe encoded protein SEQ ID NO: 28835.

XX Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; mveloma.

XX
OS Homo sapiens.
yy

PN WO200157276-A2.
XX
DD 09-AUG-2001

XX
PF 30-JAN-2001; 2001WO-US000668.
yy

PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
BP 30-JUN-2000; 2000US-00608408

PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236250P.

PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MONTANA) MONTANA DYNAMICS, INC

XX Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI ; 2001-48890/53.
XX

PT gene expression in human bone marrow.

XX

XX The present invention provides a number of single exon nucleic acid
CC

CC bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancer.

CC protein encoded by one of the probes of the invention
XX
XX

Query Match 14.0%; Score 130; DB 4; Length 163;

Matches	31;	Conservative	17;	Mismatches	43;	Indels	2;	Gaps	2;
---------	-----	--------------	-----	------------	-----	--------	----	------	----

[illegible]

Db 1 ILSHVQMLGFTVHHNNVTKMEMVLQKQKCNPAHADGCFVFCILTHGRFGAVYSSD 60

QY 137 QTHSGPLPHHRRMPMGDSCPYLAGKPKMFFIQ 169

Db 61 E--ALIPREIMSHFTALQCPLAEKPKLFFIQ 91

RESULT 6

ABG38107

ID ABG38107 standard; peptide; 163 AA.

XX ABG38107;

AC ABG38107;

XX

DT 19-AUG-2002 (first entry)

XX

DE Human peptide encoded by genome-derived single exon probe SEQ ID 27772.

XX

KW Human; single exon probe; asthma; lung cancer; COPD; ILD;

KW chronic obstructive pulmonary disease; interstitial lung disease;

KW familial idiopathic pulmonary fibrosis; neurofibromatosis;

KW tuberosus sclerosis; Gaucher's disease; Niemann-Pick disease;

KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;

KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsgener syndrome;

KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;

KW primary ciliary dyskinesia; pulmonary hypertension;

KW hyaline membrane disease.

XX

OS Homo sapiens.

XX

PN WO200186003-A2.

XX

PD 15-NOV-2001.

XX

PF 30-JAN-2001; 2001WO-US000665.

XX

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX

PA (MOLE-) MOLECULAR DYNAMICS INC.

XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX

XX WPI; 2002-114183/15.

DR

PT Spatially-addressable set of single exon nucleic acid probes, used to

PT measure gene expression in human lung samples.

XX

PS Claim 27; SEQ ID NO 27772; 634pp; English.

XX

CC The invention relates to a spatially-addressable set of single exon

CC nucleic acid probes for measuring gene expression in a sample derived

CC from human lung comprising single exon nucleic acid probes having one of

CC 12614 nucleic acid sequences mentioned in the specification, or their

CC complements or the 12387 open reading frames derived from the 12614

CC probes. Also included are a microarray comprising the novel set of probes

CC ; the novel set of probes which hybridise at high stringency to a nucleic

CC acid expressed in the human lung; measuring gene expression in a sample

CC derived from human lung, comprising (a) contacting the array with a

CC collection of detectably labeled nucleic acids derived from human lung

CC mRNA, and (b) measuring the label detectably bound to each probe of the

CC array; identifying exons in a eukaryotic genome, comprising (a)

CC algorithmically predicting at least one exon from genomic sequences of

CC the eukaryote; and (b) detecting specific hybridisation of detectably

CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,

CC having a fragment identical to the predicted exon, the probe is included

CC in the above mentioned microarray; assigning exons to a single gene,

CC comprising (a) identifying exons from genomic sequence by the method

CC above and (b) measuring the expression of each of the exons in several

CC tissues and/or cell types using hybridisation to a single exon

CC microarrays having a probe with the exon, where a common pattern of

CC expression of the exons in the tissues and/or cell types indicates that

CC the exons should be assigned to a single gene; a peptide comprising one

CC of 12011 sequences, mentioned in the specification, or encoded by the

CC probes/open reading frames (ORF). The probes are used for gene expression

CC analysis, and for identifying exons in a gene, particularly using human

CC lung derived mRNA and for the study of lung diseases such as asthma, lung

CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung

CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,

CC tuberosus sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-

CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary

CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,

CC Karsgener syndrome, fibrocystic pulmonary dysplasia, primary ciliary

CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The

CC present sequence is a peptide/protein encoded by a single exon probe of

CC the invention. Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX

XX Sequence 163 AA;

QY Query Match 14.0%; Score 130; DB 5; Length 163;

Best Local Similarity 33.3%; Pred. No. 7.7e-07;

Matches 31; Conservative 17; Mismatches 43; Indels 2; Gaps 1;

QY 77 ILRDTFTSLGYEVQKFLHLSMHGISQILGQFACMPHRDYSFVCLVSRGSGSVYQVD 136

Db 1 ILSHVQMLGFTVHHNNVTKMEMVLQKQKCNPAHADGCFVFCILTHGRFGAVYSSD 60

QY 137 QTHSGPLPHHRRMPMGDSCPYLAGKPKMFFIQ 169

Db 61 E--ALIPREIMSHFTALQCPLAEKPKLFFIQ 91

RESULT 7

AAE16024

ID AAE16024 standard; protein; 158 AA.

XX

AC AAE16024;

XX

DT 26-MAR-2002 (first entry)

XX

DE Human caspase-12 isoform, KW-F protein.

XX

KW Human; cysteine-dependent aspartate-specific proteases; caspase-12; KW-F;

KW Parkinson's disease; ulcerative colitis; cytostatic; glomerulonephritis;

KW inflammatory bowel disease; hypersensitivity; rheumatoid arthritis; ALS;

KW amyotrophic lateral sclerosis; bronchitis; inflammatory; cardiovascular;

KW neurodegenerative disease; Crohn's disease; Alzheimer's disease; cancer;

KW allergic rhinitis; cell proliferative disorder; asthma.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 40

FT /note= "Encoded by TC"

FT Misc-difference 63. .64

FT /note= "Encoded by ATGTGAGAT"

XX

XX WO200185961-A2.

PN 15-NOV-2001.

XX

PF 08-MAY-2001; 2001WO-US015103.

XX

PR 09-MAY-2000; 2000US-0203162P.

XX

PA (PHAA) PHARMACIA & UPJOHN.

XX

PI Kletzien RF, Reardon IM, Weiland KL;

XX

DR WPI; 2002-082900/11.


```
PR 13-NOV-2001; 2001US-031287P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Ruben SM;
XX WPI; 2003-175238/17.
XX New human secreted proteins and nucleic acid molecules, useful for
XX preparing a diagnostic or pharmaceutical composition for diagnosing,
XX preventing or treating cancer or other hyperproliferative disorder,
XX asthma, allergies or AIDS.
XX Claim 1; SEQ ID NO 1510; 3205pp; English.
XX The invention relates to novel genes ADA39629-ADA40565 and proteins
XX ADA40566-ADA41501 for human secreted proteins, useful for preventing,
XX treating or ameliorating medical conditions e.g. by protein or gene
XX therapy. The polypeptides, nucleic acid molecules, antibodies or their
XX fragments, and agonists or antagonists that bind to the polypeptide are
XX useful for preparing a diagnostic or pharmaceutical composition for
XX diagnosing or treating cancer or other hyperproliferative disorder. The
XX polypeptides and nucleic acid molecules are also useful for detecting,
XX preventing, diagnosing, prognosticating, treating or ameliorating cancer
XX or other hyperproliferative disorders including neoplasms, autoimmune
XX disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
XX erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
XX anaemia), haematopoietic or haematological disorders (e.g. anaemia,
XX thrombocytopenia), allergic reactions including asthma or eczema,
XX inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
XX bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
XX Alzheimer's disease or Parkinson's disease), cardiovascular disorders
XX (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
XX fungal or viral infections including HIV/AIDS), or wound healing and
XX disorders of epithelial cell proliferation. The nucleic acids are also
XX useful for chromosome identification, radiation hybrid mapping or long-
XX range restriction mapping, as molecular weight markers, or as
XX hybridization or diagnostic probes. The polypeptides and antibodies are
XX useful for providing immunological probes for differential identification
XX of the tissues immunohistochemistry assays. Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 101 AA;
SQ Query Match 7.7%; Score 71.5; DB 6; Length 101;
Best Local Similarity 27.0%; Pred. No. 4.4;
Matches 17; Conservative 10; Mismatches 19; Indels 17; Gaps 2;
QY 65 CLIIIDICIGNETELLRDFTSLGYEVQKFLHLSMHGISQILGQFA-----CMPEHR 114
DB 26 CIIIFHCVSDRSVNRRTKV-----KPVHTSVHGVGHSFVQSAPKAFKXLPVPEAVPEQK 78
QY 115 DYD 117
DB 79 DPD 81
RESULT 12
ABR47936
ID ABR47936 standard; protein; 101 AA.
XX ABR47936;
XX 12-JUN-2003 (first entry)
XX Human secreted protein, SEQ ID 827.
XX Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;
XX vulnery; antiinflammatory; nootropic; neuroprotective;
XX antiparkinsonian; gene therapy; human; cardiovascular disorder.
XX
```

```
OS Homo sapiens.
XX WO200295010-A2.
XX 28-NOV-2002.
XX 19-MAR-2002; 2002WO-US009785.
XX 21-MAR-2001; 2001US-0277340P.
XX 19-JUL-2001; 2001US-0306171P.
XX 13-NOV-2001; 2001US-0331287P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM;
XX WPI; 2003-129429/12.
XX Novel human secreted proteins, useful for detecting, preventing,
XX diagnosing, prognosticating, treating and/or ameliorating cardiovascular
XX disorders such as arrhythmia.
XX Claim 13; SEQ ID NO 827; 1881pp; English.
XX The present invention relates to novel human secreted proteins (ABR47633-
XX ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins
XX or pharmaceutical composition for diagnosing or treating a cardiovascular
XX disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary
XX arteriosclerosis and myocardial ischaemia), neural disorders, immune
XX system disorders, muscular disorders, reproductive disorders,
XX gastrointestinal disorders, pulmonary disorders, renal disorders,
XX proliferative disorders and/or cancerous diseases and conditions, for
XX wound healing and epithelial cell proliferation, to treat inflammation or
XX infection, for treating thrombosis and arteriosclerosis, for treating or
XX preventing neural damage which occurs in neuronal disorders or
XX neurodegenerative conditions such as Alzheimer's disease and Parkinson's
XX disease, to enhance bone and periodontal regeneration and aid in tissue
XX transplants or bone grafts, to prevent skin aging or hair loss, to
XX stimulate growth and differentiation of haematopoietic cells and bone
XX marrow cells when used in combination with other cytokines, to maintain
XX organs before transplantation or for supporting cell culture of primary
XX tissues, to increase or decrease differentiation or proliferation of
XX embryonic stem cells, or to modulate mammalian characteristics or
XX metabolism. Note: The sequence data for this patent was published in
XX electronic format and is available from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 101 AA;
SQ Query Match 7.7%; Score 71.5; DB 6; Length 101;
Best Local Similarity 27.0%; Pred. No. 4.4;
Matches 17; Conservative 10; Mismatches 19; Indels 17; Gaps 2;
QY 65 CLIIIDICIGNETELLRDFTSLGYEVQKFLHLSMHGISQILGQFA-----CMPEHR 114
DB 26 CIIIFHCVSDRSVNRRTKV-----KPVHTSVHGVGHSFVQSAPKAFKXLPVPEAVPEQK 78
QY 115 DYD 117
DB 79 DPD 81
RESULT 13
ABR00176
ID ABR00176 standard; protein; 101 AA.
XX ABR00176;
XX 03-APR-2003 (first entry)
XX Human gene 166 encoded secreted protein HTLEP53, SEQ ID NO:465.
XX
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Search completed: June 20, 2005, 13:41:04
Job time : 164 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 13:44:11 ; Search time 156 Seconds
(without alignments)
435.669 Million cell updates/sec

Title: US-10-713-208-6_COPY_76_252

Perfect score: 930

Sequence: 1 KQSVQAGTSYRNVLQAAIQ.....YLAGPKMFFIQNVVSDQ 177

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1013902

Minimum DB seq length: 0

Maximum DB seq length: 177

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTU5_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	166	17.8	147	14	US-10-214-932-110
2	162.5	17.5	132	17	US-10-872-079-9
3	162.5	17.5	141	17	US-10-872-079-13
4	154	16.6	167	9	US-09-864-761-48728
5	130	14.0	163	9	US-09-864-761-47950
6	108	11.6	158	10	US-09-851-873-61
7	78	8.4	134	15	US-10-114-432-32
8	78	8.4	134	15	US-10-114-432-33
9	78	8.4	146	15	US-10-114-432-7
10	78	8.4	146	15	US-10-114-432-20
11	78	8.4	146	15	US-10-114-432-65

12	78	8.4	146	15	US-10-114-432-70	Sequence 70, Appl
13	78	8.4	174	15	US-10-114-432-34	Sequence 34, Appl
14	77	8.3	52	9	US-09-989-903-51	Sequence 51, Appl
15	77	8.3	52	14	US-10-068-564-51	Sequence 51, Appl
16	77	8.3	52	16	US-10-870-765-51	Sequence 51, Appl
17	76	8.2	56	9	US-09-989-903-58	Sequence 58, Appl
18	76	8.2	56	14	US-10-068-564-58	Sequence 58, Appl
19	76	8.2	56	16	US-10-870-765-58	Sequence 58, Appl
20	75.5	8.1	74	9	US-09-989-903-18	Sequence 18, Appl
21	75.5	8.1	74	14	US-10-068-564-18	Sequence 18, Appl
22	75.5	8.1	74	16	US-10-870-765-18	Sequence 18, Appl
23	75.5	8.1	77	9	US-09-989-903-25	Sequence 25, Appl
24	75.5	8.1	77	14	US-10-068-564-25	Sequence 25, Appl
25	75.5	8.1	77	16	US-10-870-765-25	Sequence 25, Appl
26	74.5	8.0	94	9	US-09-989-903-14	Sequence 14, Appl
27	74.5	8.0	94	14	US-10-068-564-14	Sequence 14, Appl
28	74.5	8.0	94	16	US-10-870-765-14	Sequence 14, Appl
29	73	7.8	39	8	US-08-459-455-45	Sequence 45, Appl
30	71.5	7.7	101	15	US-10-653-595-149	Sequence 149, App
31	71.5	7.7	102	10	US-09-397-945-149	Sequence 149, App
32	70	7.5	51	9	US-09-989-903-45	Sequence 45, Appl
33	70	7.5	51	14	US-10-068-564-45	Sequence 45, Appl
34	70	7.5	51	16	US-10-870-765-45	Sequence 45, Appl
35	68	7.3	39	9	US-09-989-903-38	Sequence 38, Appl
36	68	7.3	39	14	US-10-068-564-38	Sequence 38, Appl
37	68	7.3	39	16	US-10-870-765-38	Sequence 38, Appl
38	66.5	7.2	102	11	US-09-864-408A-1582	Sequence 1582, Ap
39	66	7.1	39	9	US-09-989-903-30	Sequence 30, Appl
40	66	7.1	39	14	US-10-068-564-30	Sequence 30, Appl
41	66	7.1	39	16	US-10-870-765-30	Sequence 30, Appl
42	66	7.1	167	15	US-10-429-872-20	Sequence 20, Appl
43	65.5	7.0	130	15	US-10-424-593-271119	Sequence 271119,
44	64.5	6.9	141	15	US-10-424-593-231330	Sequence 231330,
45	64.5	6.9	174	15	US-10-282-122A-76633	Sequence 76633, A

ALIGNMENTS

RESULT 1

US-10-214-932-110
; Sequence 110, Application US/10214932
; Publication No. US20030100707A1
; GENERAL INFORMATION:
; APPLICANT: HWANG, Inhan
; APPLICANT: KIM, Dae Heon
; APPLICANT: LEE, Yong Jik
; TITLE OF INVENTION: SYSTEM FOR DETECTING PROTEASE
; FILE REFERENCE: APB02/US
; CURRENT APPLICATION NUMBER: US/10/214,932
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 110
; TYPE: PRT
; LENGTH: 147
; ORGANISM: Homo sapiens
US-10-214-932-110

Query Match	17.8%	Score 166;	DB 14;	Length 147;
Best Local Similarity	32.8%	Pred. No. 9.9e-10;		
Matches	43;	Conservative	22;	Mismatches 49;
				Indels 18;
				Gaps 4;
QY	52	EERYKMKSKPLGICLIID-----CIGNETEL--LRDTFTSLGYEVQKFLHLSM	97	
Db	6	DNSYKMDYEMGLICIIINKNFKHKTGMSRSCDVAANLRRETFRLKYEVKNKDLTR	65	
QY	98	HGISQILQGFACMPERHDVDSFVCLVSRGGSOSVGDVTHSGLPLHHRFMGDSCP	157	
Db	66	EIVELMRDVS-KEDHSKRSFVCLLSHGEIGIFG---TNGPVLKKITNFRGDRCR	121	
QY	158	YLAGKPKMFFIQ 169		

Db 122 SLTGKPKLFIIQ 133

RESULT 2

US-10-872-079-9
; Sequence 9, Application US/10872079
; Publication No. US20050095613A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-280001
; CURRENT APPLICATION NUMBER: US/10/872,079
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/573,641
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: US 60/180,021
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-872-079-9

Query Match 17.5%; Score 162.5; DB 17; Length 132;
Best Local Similarity 40.0%; Pred. No. 2.1e-09;
Matches 42; Conservative 13; Mismatches 41; Indels 9; Gaps 2;

QY 74 ETELLRDTFTSLGYEVQKFLHLSMHGISOILGOFACMPBHRDYDSFVCLVSRGGSQ--- 130
DB 19 DAENLRLFRSLGYEVKVKNDLTAEMVCLKRFKREBHKDSDFVLVLLSHGEEHILQ 78

QY 131 ---SVYGVGD---QTHSGPLPHHIRMFGMDCSPYLAGPKPMFFIQ 169
DB 79 FPGGIYGTGKEKVPDILSLKFIKFNLFNGDNCPSLKGKPKLFIIQ 123

RESULT 3

US-10-872-079-13
; Sequence 13, Application US/10872079
; Publication No. US20050095613A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-280001
; CURRENT APPLICATION NUMBER: US/10/872,079
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/573,641
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: US 60/180,021
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-872-079-13

Query Match 17.5%; Score 162.5; DB 17; Length 141;
Best Local Similarity 40.0%; Pred. No. 2.3e-09;
Matches 42; Conservative 13; Mismatches 41; Indels 9; Gaps 2;

QY 74 ETELLRDTFTSLGYEVQKFLHLSMHGISOILGOFACMPBHRDYDSFVCLVSRGGSQ--- 130
DB 28 DAENLRLFRSLGYEVKVKNDLTAEMVCLKRFKREBHKDSDFVLVLLSHGEEHILQ 87

QY 131 ---SVYGVGD---QTHSGPLPHHIRMFGMDCSPYLAGPKPMFFIQ 169
DB 88 FPGGIYGTGKEKVPDILSLKFIKFNLFNGDNCPSLKGKPKLFIIQ 132

RESULT 4

US-09-864-761-48728
; Sequence 48728, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48728
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007256.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EST HUMAN HIT: BE271526.1, EVALUE 2.00e-98
; OTHER INFORMATION: SWISSPROT HIT: Q14790, EVALUE 2.00e-99
US-09-864-761-48728

Query Match 16.6%; Score 154; DB 9; Length 167;
Best Local Similarity 35.4%; Pred. No. 2.4e-08;
Matches 35; Conservative 18; Mismatches 38; Indels 8; Gaps 3;

QY 78 LRDTFTSLGVEYQKFLHLSMHGISOILQGFACMPEDRDYDFVCLVSRGSGSQSVYGVDDQ 137
Db 2 LTTTEELHFEKPHDDCTVEQIYELLYQLM-DHSNMDCFICILSHGDKGIYGTGD 60
QY 138 THSGPLHHRMFMDGSCPYLAGPKMFFIQ-----NY 171
Db 61 QEA--PIVELTSQFTGLKCPSLAGPKVFFIQACQGDNY 97

RESULT 5

US-09-864-761-47950
; Sequence 47950, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aomicca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47950
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007283.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.1
; OTHER INFORMATION: EST HUMAN HIT: BE271526.1, EVALUE 4.00e-31
; OTHER INFORMATION: SWISSPROT HIT: Q92851, EVALUE 3.00e-94
US-09-864-761-47950

Query Match 14.0%; Score 130; DB 9; Length 163;
Best Local Similarity 33.3%; Pred. No. 9.7e-06;
Matches 31; Conservative 17; Mismatches 43; Indels 2; Gaps 1;
QY 77 LRDTFTSLGVEYQKFLHLSMHGISOILQGFACMPEDRDYDFVCLVSRGSGSQSVYGVDD 136
Db 1 ILSHVFQMLGFTVHTNNVTKVEMEMVLQKQKCNPAHADGDCFVFCILTHGRFGAVYSSD 60
QY 137 QTHSGPLHHRMFMDGSCPYLAGPKMFFIQ 169
Db 61 E--ALIPIREINSHFTALQCPRLAEKPKLFFTIQ 91

RESULT 6

US-09-851-873-61
; Sequence 61, Application US/09851873
; Publication No. US20030165488A1
; GENERAL INFORMATION:
; APPLICANT: Kletzien, Rolf F
; APPLICANT: Reardon, Ilene M
; APPLICANT: Welland, Katherine L
; TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
; FILE REFERENCE: 28341/00233
; CURRENT APPLICATION NUMBER: US/09/851,873
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 61
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-873-61

Query Match 11.6%; Score 108; DB 10; Length 158;
Best Local Similarity 26.4%; Pred. No. 0.0023;
Matches 42; Conservative 19; Mismatches 70; Indels 28; Gaps 4;
QY 26 PSNFRFPVKKSIOSEAFLPQSIPEERYKMKSPGLGCLIDC-----IGNE 74
Db 11 PHAHFHELTGRA-----DEIYPVMEKERTCLALNTRNKEFNVLHNRNGSE 57
QY 75 TELL--RDTFTSLGVEYQKFLHLSMHGISOILQGFACMPEDRDYDFVCLVSRGSGSQSV 133
Db 58 LLLGLMDLLENLGVSVIKESLTAEOMETALRQFAHPEHQSSDTFLVFMHSHILNGIC 117
QY 134 GV---DQTHSGPLHHRMFMDGSCPYLAGPKMFFIQ 169
Db 118 GTKHWDQPDVLDHDDTIFEINRNCQSLKDKPKVIMQ 156

RESULT 7

US-10-114-432-32
; Sequence 32, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Sid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 134
; TYPE: PRT

100

100

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; SEQ ID NO 51
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-989-903-51

Query Match      8.3%; Score 77; DB 9; Length 52;
Best Local Similarity 50.0%; Pred. No. 1.3;
Matches 13; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 144 LHHRRMFMGDSCPYLAGKPKMFFIQ 169
   ::: ||| :|||:||||
Db 4 IYDLTSYFTGSKCPSLSGKPKIFFIQ 29

RESULT 15
US-10-068-564-51
; Sequence 51, Application US/10068564
; Publication No. US20030040096A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C2
; CURRENT APPLICATION NUMBER: US/10/068,564
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-068-564-51

Query Match      8.3%; Score 77; DB 14; Length 52;
Best Local Similarity 50.0%; Pred. No. 1.3;
Matches 13; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 144 LHHRRMFMGDSCPYLAGKPKMFFIQ 169
   ::: ||| :|||:||||
Db 4 IYDLTSYFTGSKCPSLSGKPKIFFIQ 29

Search completed: June 20, 2005, 13:57:30
Job time : 157 secs
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Result No.	Query			ID	Description	
	Score	Match	Length			
1	166	17.8	148	3	US-08-964-308-11	Sequence 11, Appl
2	166	17.8	148	3	US-08-964-313-11	Sequence 11, Appl
3	186	17.8	148	3	US-09-069-138-11	Sequence 61, Appl
4	108	11.6	158	4	US-09-851-873-61	Sequence 51, Appl
5	77	8.3	52	3	US-09-187-789-51	Sequence 46, Appl
6	77	8.3	52	4	US-09-139-600-46	Sequence 51, Appl
7	77	8.3	52	4	US-09-989-903-51	Sequence 58, Appl
8	76	8.2	56	3	US-09-187-789-58	Sequence 53, Appl
9	76	8.2	56	4	US-09-139-600-53	Sequence 58, Appl
10	76	8.2	56	4	US-09-989-903-58	Sequence 18, Appl
11	75.5	8.1	74	3	US-09-187-789-18	Sequence 13, Appl
12	75.5	8.1	74	4	US-09-139-600-13	Sequence 25, Appl
13	75.5	8.1	74	4	US-09-989-903-18	Sequence 20, Appl
14	75.5	8.1	77	3	US-09-187-789-25	Sequence 35, Appl
15	75.5	8.1	77	3	US-09-139-600-20	Sequence 23, Appl
16	75.5	8.1	77	4	US-09-989-903-25	Sequence 33680, A
17	75	8.1	147	4	US-09-270-767-33680	Sequence 48897, A
18	75	8.1	147	4	US-09-270-767-48897	Sequence 14, Appl
19	74.5	8.0	94	3	US-09-187-789-14	Sequence 9, Appl
20	74.5	8.0	94	4	US-09-139-600-9	Sequence 14, Appl
21	74.5	8.0	94	4	US-09-989-903-14	Sequence 46, Appl
22	73	7.8	39	3	US-08-258-287B-46	Sequence 45, Appl
23	73	7.8	39	3	US-08-368-704C-45	Sequence 3337, Ap
24	70.5	7.6	173	3	US-09-540-236-3337	Sequence 45, Appl
25	70	7.5	51	3	US-09-187-789-45	Sequence 40, Appl
26	70	7.5	51	4	US-09-139-600-40	Sequence 45, Appl
27	70	7.5	51	4	US-09-989-903-45	

Db 7 DMSYKMDYPEMGLCIIINNKNFHKSTGMTSGTVDVDAANLRETFRNLKYEVRNKNLDR 66
QY 98 HGISQILGQACMPHEHRDYSFVCLVSRGGSQSVYGVDTHTSGLPLHHRMFMGDS 157
Db 67 EEIVELMRDVS-KEDHSKRSSFVCLLSHGEGIIIFG---TNGPVDLKKITNFFRGDR 122
QY 158 YLAGPKPMFFIQ 169
Db 123 SLTGPKPLFIQ 134

RESULT 2
US-08-964-313-11
; Sequence 11, Application US/08964313
; Patent No. 6114132
; GENERAL INFORMATION:
; APPLICANT: DESMARAIS, SYLVIE
; APPLICANT: FRIESEN, RICHARD
; APPLICANT: GRESSER, MICHAEL
; APPLICANT: KENNEDY, BRIAN
; APPLICANT: NICHOLSON, DONALD
; APPLICANT: RAMACHANDRAN, CHIDAMBARAN
; APPLICANT: SKOREY, KATHRYN
; APPLICANT: FORD-HUTCHINSON, ANTHONY
; TITLE OF INVENTION: PHOSPHATASE BINDING ASSAY
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,313
; FILING DATE: 04-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,408
; FILING DATE: 04-NOV-1996
; APPLICATION NUMBER: PCT/CA97/00825
; FILING DATE: 03-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: DURETTE, PHILIPPE L.
; REGISTRATION NUMBER: 35,125
; REFERENCE/DOCKET NUMBER: 19824Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-4568
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-964-313-11

Query Match 17.8%; Score 166; DB 3; Length 148;
Best Local Similarity 32.6%; Pred. No. 2.1e-12;
Matches 43; Conservative 22; Mismatches 49; Indels 18; Gaps 4;

QY 52 EERYKMKSKPLGICLIID-----CIGNETEL--LRDTFTSLGYEVQKFLHLSM 97
Db 7 DMSYKMDYPEMGLCIIINNKNFHKSTGMTSGTVDVDAANLRETFRNLKYEVRNKNLDR 66

QY 98 HGISQILGQACMPHEHRDYSFVCLVSRGGSQSVYGVDTHTSGLPLHHRMFMGDS 157
Db 67 EEIVELMRDVS-KEDHSKRSSFVCLLSHGEGIIIFG---TNGPVDLKKITNFFRGDR 122
QY 158 YLAGPKPMFFIQ 169
Db 123 SLTGPKPLFIQ 134

Db 67 EEIVELMRDVS-KEDHSKRSSFVCLLSHGEGIIIFG---TNGPVDLKKITNFFRGDR 122
QY 158 YLAGPKPMFFIQ 169
Db 123 SLTGPKPLFIQ 134

RESULT 3
US-09-069-138-11
; Sequence 11, Application US/09069138
; Patent No. 6348572
; GENERAL INFORMATION:
; APPLICANT: DESMARAIS, SYLVIE
; APPLICANT: DUFRESNE, CLAUDE
; APPLICANT: FRIESEN, RICHARD
; APPLICANT: LEBLANC, YVES
; APPLICANT: ROY, PATRICK
; APPLICANT: YOUNG, ROBERT N.
; APPLICANT: ZAMBONI, ROBERT
; TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,138
; FILING DATE: 29-APR-1998
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: DURETTE, PHILIPPE L.
; REGISTRATION NUMBER: 35,125
; REFERENCE/DOCKET NUMBER: 19840YIA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-4568
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-069-138-11

Query Match 17.8%; Score 166; DB 3; Length 148;
Best Local Similarity 32.6%; Pred. No. 2.1e-12;
Matches 43; Conservative 22; Mismatches 49; Indels 18; Gaps 4;

QY 52 EERYKMKSKPLGICLIID-----CIGNETEL--LRDTFTSLGYEVQKFLHLSM 97
Db 7 DMSYKMDYPEMGLCIIINNKNFHKSTGMTSGTVDVDAANLRETFRNLKYEVRNKNLDR 66

QY 98 HGISQILGQACMPHEHRDYSFVCLVSRGGSQSVYGVDTHTSGLPLHHRMFMGDS 157
Db 67 EEIVELMRDVS-KEDHSKRSSFVCLLSHGEGIIIFG---TNGPVDLKKITNFFRGDR 122
QY 158 YLAGPKPMFFIQ 169
Db 123 SLTGPKPLFIQ 134

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RESULT 4
US-09-851-873-61
; Sequence 61, Application US/09851873
; Patent No. 6833248
; GENERAL INFORMATION:
; APPLICANT: Kletzien, Rolf F
; APPLICANT: Reardon, Ilene M
; APPLICANT: Weiland, Katherine L
; TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
; FILE REFERENCE: 28341/00233
; CURRENT APPLICATION NUMBER: US/09/851,873
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-873-61

Query Match      11.6%; Score 108; DB 4; Length 158;
Best Local Similarity 26.4%; Pred. No. 3.9e-05;
Matches 42; Conservative 19; Mismatches 70; Indels 28; Gaps 4;

QY 26 PSNNFREPEVKIGQSEAFLOSIPEERYKMKSKPLGICLIIDC-----IGNE 74
DB 11 PHAFPHLKTGRA-----DEIYPVMEKERTCLALNIRNKEFNLYLNRNGSE 57

QY 75 TELL-RDTFTSLGYEVOKFLHLSMHGISQILGQFACMPHEHDYDSFVCVLVSRGSGSQSVY 133
DB 58 LDLLGMDLLENLGYSVVVIESLTAQEMETALRQFAAHPHQSSDSTFLVFMHSIILNGIC 117

QY 134 GV---DOTHGCLPLHRRFMFGDSCPYLAGKPKMFFIQ 169
DB 118 GTKHWQEPDVLHDDTIFEIFNRRNCQSLKDKPKVIIMQ 156

RESULT 5
US-09-187-789-51
; Sequence 51, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-51

Query Match      8.3%; Score 77; DB 3; Length 52;
Best Local Similarity 50.0%; Pred. No. 0.052;
Matches 13; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 144 LHHRMFMDGDCPYLAGKPKMFFIQ 169
DB 4 IYDLTSYFTGSKCPSLSGKPKIFFIQ 29

RESULT 6
US-09-139-600-46
; Sequence 46, Application US/09139600
; Patent No. 6432628
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-58

Query Match      8.2%; Score 76; DB 3; Length 56;
Best Local Similarity 53.6%; Pred. No. 0.077;

QY 144 LHHRMFMDGDCPYLAGKPKMFFIQ 169
DB 4 IYDLTSYFTGSKCPSLSGKPKIFFIQ 29

RESULT 7
US-09-989-903-51
; Sequence 51, Application US/09989903
; Patent No. 6797812
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434D1
; CURRENT APPLICATION NUMBER: US/09/989,903
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-989-903-51

Query Match      8.3%; Score 77; DB 4; Length 52;
Best Local Similarity 50.0%; Pred. No. 0.052;
Matches 13; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 144 LHHRMFMDGDCPYLAGKPKMFFIQ 169
DB 4 IYDLTSYFTGSKCPSLSGKPKIFFIQ 29

RESULT 8
US-09-187-789-58
; Sequence 58, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-58

Query Match      8.2%; Score 76; DB 3; Length 56;
Best Local Similarity 53.6%; Pred. No. 0.077;
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; LENGTH: 74
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-989-903-18
Query Match 8.1%; Score 75.5; DB 4; Length 74;
Best Local Similarity 30.6%; Pred. No. 0.14;
Matches 19; Conservative 11; Mismatches 29; Indels 3; Gaps 1;
QY 111 PEHRDYDSFVCVLVSRGGSQSVGVQDTHSGPLPHH---IRRPMFGDSCPYLAGKPKMFF 167
Db 1 PEHQSSDSTPLVFMHSHGILGICGVKRNKPDVLHDDTIFKIFNNSNCKSLRNKPKILI 60
QY 168 IQ 169
Db 61 MQ 62

RESULT 14
US-09-187-789-25
; Sequence 25, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-25

Query Match 8.1%; Score 75.5; DB 3; Length 77;
Best Local Similarity 34.4%; Pred. No. 0.14;
Matches 22; Conservative 8; Mismatches 27; Indels 7; Gaps 2;
QY 111 PEHRDYDSFVCVLVSRGGSQSVGVQDTHSG---LPLHHIRRMFMGDSCPYLAGKPKM 165
Db 1 PEHKTSDSTPLVFMHSHGICGICGT--TYSNEVSDILKVDITIFQMMNTLKCPSLKDKPKV 58
QY 166 FFIQ 169
Db 59 IIIQ 62

RESULT 15
US-09-139-600-20
; Sequence 20, Application US/09139600
; Patent No. 6432628
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHOD OF USE
; FILE REFERENCE: 480140.434
; CURRENT APPLICATION NUMBER: US/09/139,600
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-20

Query Match 8.1%; Score 75.5; DB 4; Length 77;
Best Local Similarity 34.4%; Pred. No. 0.14;

Matches 22; Conservative 8; Mismatches 27; Indels 7; Gaps 2;
QY 111 PEHRDYDSFVCVLVSRGGSQSVGVQDTHSG---LPLHHIRRMFMGDSCPYLAGKPKM 165
Db 1 PEHKTSDSTPLVFMHSHGICGICGT--TYSNEVSDILKVDITIFQMMNTLKCPSLKDKPKV 58
QY 166 FFIQ 169
Db 59 IIIQ 62

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Job time : 43 secs

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OM protein - protein search, using sw model

Run on: June 20, 2005, 13:53:52 ; Search time 38 Seconds
(without alignments) 243.074 Million cells

Title: US-10-713-208-6_COPY_253_348
 Perfect score: 497
 Sequence: 1 LEDSLLLEVDGPMKQNVFK.....ITESKMHFSSLCILLDLVL 96

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 34996

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Minimum DB seq length: 0
Maximum DB seq length: 96
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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PIR_1: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Match	Length			
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2	49	9.9	74	2	AG2533	hypothetical prote
3	48.5	9.8	68	2	AD2173	hypothetical prote
4	48.5	9.8	96	2	G33730	Ig kappa chain V r
5	48	9.7	51	2	H82689	hypothetical prote
6	47.5	9.6	65	1	XTPQ1	acrosin inhibitor
7	47.5	9.6	71	2	S20194	sperm-associated a
8	47.5	9.6	85	2	F86389	probable DNA-bind
9	47.5	9.6	92	2	A26395	T-cell receptor be
10	46	9.3	42	2	T07285	hypothetical prote
11	46	9.3	69	2	PH1080	Ig light chain V r
12	46	9.3	80	2	T01450	limonene cyclase h
13	46	9.3	87	2	A64429	hypothetical prote
14	45.5	9.2	69	2	E25647	hypothetical lc pr
15	44.5	9.0	58	2	AC1869	hypothetical prote
16	44.5	9.0	72	2	E43259	H+-transporting tw
17	44.5	9.0	88	2	S66287	saeacin B precursor
18	44.5	9.0	92	2	AB2021	hypothetical prote
19	44	8.9	68	2	C97874	degenerate transp
20	44	8.9	72	2	T31010	hypothetical prote
21	43.5	8.8	60	2	S68769	short neurotoxin -
22	43.5	8.8	82	2	T04476	acclimation protei
23	43.5	8.8	84	2	T17637	hypothetical prote
24	43	8.7	66	2	H82783	hypothetical prote
25	43	8.7	67	2	B35063	hypothetical prote
26	43	8.7	71	2	T29378	LuN-32 protein - C
27	43	8.7	92	2	AF1919	hypothetical prote
28	43	8.7	96	2	T45337	hypothetical prote
29	42.5	8.6	58	2	B43928	probable collagen

Query Match 9.9%; Score 49; DB 2; Length 74;
Best Local Similarity 47.6%; Pred. No. 1.2e+02;
Matches 10; Conservative 2; Mismatches 7; Indels

ALIGNMENTS

RESULT 1

040621.1
 S44828
 F54P2.3 protein - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
 C;Accession: S44828
 R;Anderson, K.
 submitted to the EMBL Data Library, September 1993
 A;Description: Sequence of the *C. elegans* cosmid P54F2.
 A;Reference number: S44817
 A;Accession: S44828
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-34 <AND>
 A;Cross-references: EMBL:L23645; NID:G388603; PID:G388609
 C;Genetics:
 A;Introns: 20/1

Query Match 10.1%; Score 50; DB 2; Length 34;
Best Local Similarity 29.4%; Pred. No. 38;
Matches 10: Conservative 9; Mismatches 15; Indels 0; Gaps 0;

RESULT 2

AG3533
 hypothetical protein asr7554 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120bet
 C/Species: Nostoc sp. PCC 7120
 A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C/Accession: AG2533
 R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Kanazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
 A/Reference number: AB1807; MUID:21595285; PMID:11759840
 A/Accession: AG2533
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-74 <KUR>
 A/Cross-references: UNIPROT:Q8ZSF6; GB:AP003602; PIDN:BAB77197.1; PID:gl7134639; GSPDB:GN
 A/Experimental source: strain PCC 7120
 C/Genetics:
 A/Gene: asr7554
 A/Genome: plasmid

Oy **25** GLCTVHREADF--FWSLCTAD 43
 |:|||||:|:
Dd **12** GICTFHNADFVKFCQVCNFD 32
 |:|||||:|:

RESULT 3

AD2173
hypothetical protein asr2939 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A>Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AD2173
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AD2173
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-68 <KUR>
A:Cross-references: UNIPROT:OBYSZ0; GB:BA000019; PIDN:BAB74639.1; PID:g17132033; GSPDB:C
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: asr2939

Query Match 9.8%; Score 48.5; DB 2: Length 68;
Best Local Similarity 36.1%; Pred.No. 1.3e+02;
Matches 13; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

Oy **50** SHSPSLYLQLCSOKLRQRGTIPGSGITES-KDMH 84
 |:||::|:|||||:
Dd **15** STAKPWLVLQLRLKKLQEHRDTIPANVYAEELADIH 50
 |:||::|:|||||:

RESULT 4

G33730
Ig kappa chain V region (23.32) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C:Accession: G33730
R:Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A>Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unli
A:Reference number: A33730; MUID:89367325; PMID:2505260
A:Accession: G33730
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-96 <LAW>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 9.8%; Score 48.5; DB 2: Length 96;
Best Local Similarity 29.5%; Pred. No. 1.9e+02;
Matches 13; Conservative 7; Mismatches 17; Indels 7; Gaps 1;

Oy **40** CTADMSL-----LEQHSSPSLYLQLCSOKLRQRGTIPGSG 76
 |:||:|:|:|:|:|:|:
Dd **23** CRASQSISDLHWYQQKHSHESPLLIKYASQSISGIPSFRGS 66
 |:||:|:~::~|:|:|:|:|:|:

RESULT 5

H82689
hypothetical protein XF1364 [imported] - Xylella fastidiosae (strain 9aSc)
C:Species: Xylella fastidiosae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: H82689
R:Anonymous, The Xylella fastidiosae Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A>Title: The genome sequence of the plant pathogen Xylella fastidiosae.
A:Reference number: AB2515; MUID:20365717; PMID:10910347

A:Accession: S20394
A:Molecule type: protein
A:Residues: 1-71 <JON>
A:Experimental source: spermatozoa
A:Accession: S20395
A:Molecule type: protein
A:Residues: 3-68 <J02>
A:Experimental source: spermatozoa
A:Note: these proteins were not glycosylated
R:Calvete, J.J.; Dostalova, Z.; Sanz, L.; Adermann, K.; Thole, H.H.; Toepfer-Petersen, H.
FEBS Lett. 379, 207-211, 1996
A:Title: Mapping the heparin-binding domain of boar spermadhesins.
A:Reference number: S68648; MUID:96184566; PMID:8603690
A:Accession: S68652
A:Molecule type: protein
A:Residues: 1-11, 'X', 13, 18-21, 'X', 23-26 <CAL>
C:Superfamily: pancreatic secretory trypsin inhibitor; Kazal proteinase inhibitor homolog
C:Keywords: semen; serine proteinase inhibitor; sperm; testis
F:1-71/Product: sperm-associated acrosin inhibitor, minor form #status experimental <WAT>
F:1-68, 70-71/Product: sperm-associated acrosin inhibitor, long form #status experimental
F:3-68, 70-71/Product: sperm-associated acrosin inhibitor, short form #status experimental
F:10-62/Domain: Kazal proteinase inhibitor homology <XPI>
F:12-44, 22-41, 30-62/Disulfide bonds: #status experimental
F:50/Inhibitory site: Arg (acrosin, trypsin) #status predicted

Query Match 9.6%; Score 47.5; DB 2; Length 71;
Best Local Similarity 30.9%; Pred. No. 1.7e+02;
Matches 17; Conservative 12; Mismatches 15; Indels 11; Gaps 4;

QY 20 KAKRGGLCTVHREADFWSLCTADMSLL----EQSHSSPSLYLQCLSKL-ROER 69
Db 5 KTRKEPDCDVRSHLFF---CTREMPICGTNGKSYANPCIF--CSEKLGKNEK 53

RESULT 8
F86389
probable DNA-binding protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: F86389
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.E.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Rozenberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F86389
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-85 <STO>
A:Cross-references: UNIPROT:Q9C676; GB:AE005172; NID:gl1079506; PIDN:AG29217.1; GSPDB:G
C:Genetics:
A:Map position: 1
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

Query Match 9.6%; Score 47.5; DB 2; Length 85;
Best Local Similarity 28.3%; Pred. No. 2.1e+02;
Matches 13; Conservative 10; Mismatches 20; Indels 3; Gaps 1;

QY 6 LLEVDGPMKNVFFKAKRGGLCTVHREADFWSLCTADMSLLRQSH 51
Db 8 LKRIENKINQVTFKRRTGLL---KKAQEIISVLCDAEIVLIVFSH 50

RESULT 9
A26395
T-cell receptor beta chain V-D-J-C0 regions (NZW8) - mouse (fragment)
C:Species: Mus musculus (house mouse)

C:Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 30-May-1997
C:Accession: A26395
R:Behlke, M.A.; Loh, D.Y.
Nature 322, 379-382, 1986
A:Title: Alternative splicing of murine T-cell receptor beta-chain transcripts.
A:Reference number: A26395; MUID:86284983; PMID:3488509
A:Accession: A26395
A:Molecule type: mRNA
A:Residues: 1-92 <BEH>
A:Cross-references: GB:M30880
A:Note: alternative splicing gives rise to transcripts containing an additional exon betw
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 9.6%; Score 47.5; DB 2; Length 92;
Best Local Similarity 30.0%; Pred. No. 2.3e+02;
Matches 27; Conservative 6; Mismatches 26; Indels 31; Gaps 6;

QY 5 SLLEVDGPMKNVFFKAKRG-----LCTVHREADFFWS---LCT 41
Db 7 SLME-DGGAFKD-RFKAEMLNSSFTLKIQTEPKDSAVYLCASTRATEVFFGKGRLLTV 64

QY 42 ADMSLLEQSHSSPSLYLQCLSKLROERG 71
Db 65 VGLRLSYASHHS-SLTSQC-----RSECGT 88

RESULT 10
T07285
hypothetical protein 42b - Chlorella vulgaris chloroplast
C:Species: Chlorella vulgaris
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C:Accession: T07285
R:Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, S.; Tsudzuki, J.; Nakas
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A:Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlo
A:Reference number: Z15985; MUID:97303241; PMID:9159184
A:Accession: T07285
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-42 <WAK>
A:Cross-references: EMBL:AB001684; NID:g2224352; PIDN:BAA57933.1; PID:g2224449
C:Genetics:
C:Keywords: chloroplast

Query Match 9.3%; Score 46; DB 2; Length 42;
Best Local Similarity 28.2%; Pred. No. 1.4e+02;
Matches 11; Conservative 9; Mismatches 9; Indels 10; Gaps 1;

QY 48 EQSHSSPSLYLQCLSKLROERGTFPGSGITESKDMHFS 86
Db 8 KKSQYTCQSYLTIVDQELSEE-----BEEDWFFS 36

RESULT 11
PH1080
Ig light chain V region (clone 165.60) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C:Accession: PH1080
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B ce
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1080
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-69 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match		9.3%; Score 46; DB 2; Length 69;
Best Local Similarity		28.0%; Pred. No. 2.5e+02;
Matches		14; Conservative 6; Mismatches 18; Indels 12; Gaps 1;
QY	48 ESHSPSLYLQCLSQKLRQERTIPGSGI-----TESKDMHF 85	
DB	9 QKSHESPLLIKYASOSTISGIPRFGSGGDTFLSINSVETDFGMVF 58	
RESULT 12		
T01450		
lmonene cyclase homolog F2401.12 - Arabidopsis thaliana		
C:Species: Arabidopsis thaliana (mouse-ear cress)		
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 15-Mar-2004		
C:Accession: T01450		
R:Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Con		
eologis, A.; Ecker, J.R.		
submitted to the EMBL Data Library, January 1998		
A:Description: Genomic sequence for Arabidopsis thaliana BAC F2401.		
A:Reference number: Z14211		
A:Accession: T01450		
A>Status: translated from GB/EMBL/DBDJ		
A:Molecule type: DNA		
A:Residues: 1-80 <SHI>		
A:Cross-references: EMBL:AC003113; NID:g2689438; PID:g2781356; GSPDB:GN00059; ATSP:F2401		
A:Experimental source: cultivar Columbia		
C:Genetics:		
A:Gene: ATSP:F2401.12		
A:Map position: 1		
C:Superfamily: vetispiradiene synthase 1		
Query Match		9.3%; Score 46; DB 2; Length 80;
Best Local Similarity		26.5%; Pred. No. 3e+02;
Matches		9; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
QY	49 QSHSPSLYLQCLSQKLRQERTIPGSGITESKD 82	
DB	37 KSPSLPERLIKMDKNVRNLSTMGCGLVKYND 70	
RESULT 13		
A64429		
hypothetical protein MJ1034 - Methanococcus jannaschii		
C:Species: Methanococcus jannaschii		
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004		
C:Accession: A64429		
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, A.		
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.		
; Raon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.		
Science 273, 1058-1073, 1996		
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C		
A>Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii		
A:Reference number: A64300; MUID:96337999; PMID:8688087		
A:Accession: A64429		
A>Status: preliminary; nucleic acid sequence not shown; translation not shown		
A:Molecule type: DNA		
A:Residues: 1-87 <BUL>		
A:Cross-references: UNIPROT:Q58440; GB:U67546; GB:L77117; NID:g1591687; PIDN:ARB999038.1;		
C:Genetics:		
A:Map position: FOR966052-966315		
C:Superfamily: conserved hypothetical protein MJ1034		
Query Match		9.3%; Score 46; DB 2; Length 87;
Best Local Similarity		26.3%; Pred. No. 3.3e+02;
Matches		10; Conservative 12; Mismatches 12; Indels 4; Gaps 2;
QY	7 LEVDGPAMKNVEFKAQKGL-CTVHREADF---FWSLC 40	
DB	24 LAIEKPSLKIDIEKALKKLGLEPKIYRKRYPRQHWIEIC 61	
RESULT 14		
E25647		

hypothetical lc protein - phage PA2		
C:Species: phage PA2		
A>Note: host Escherichia coli		
C>Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 09-Jul-2004		
C:Accession: E25647		
R:Blasband, A.J.; Marcotte Jr., W.R.; Schnaitman, C.A.		
J. Biol. Chem. 261, 12723-12732, 1986		
A>Title: Structure of the lc and nmpC outer membrane porin protein genes of lambdoid bact		
A:Reference number: A25647; MUID:86304457; PMID:3017988		
A:Accession: E25647		
A:Molecule type: DNA		
A:Residues: 1-69 <BLA>		
A:Cross-references: UNIPROT:Q38586; GB:J02580; NID:g215366; PIDN:AAA32302.1; PID:g215370		
Query Match		9.2%; Score 45.5; DB 2; Length 69;
Best Local Similarity		22.2%; Pred. No. 2.9e+02;
Matches		12; Conservative 16; Mismatches 21; Indels 5; Gaps 2;
QY	44 MSLRLQSHSP--SLYLQCLSQKLRQERTIPGSGITESKDMHFSLGCLILDV 95	
DB	17 LELVNQTYSDNVISAYTECFSEVIFVKQVDFV---INESRHIFVEVIGCTYINI 67	
RESULT 15		
AC1869		
hypothetical protein asr0500 [imported] - Nostoc sp. (strain PCC 7120)		
C:Species: Nostoc sp. PCC 7120		
A>Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120		
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004		
C:Accession: AC1869		
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,		
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.		
DNA Res. 8, 205-213, 2001		
A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anat		
A:Reference number: AB1807; MUID:21595285; PMID:11759840		
A:Accession: AC1869		
A>Status: preliminary		
A:Molecule type: DNA		
A:Residues: 1-58 <KUR>		
A:Cross-references: UNIPROT:Q8YZG0; GB:BA000019; PIDN:BA872458.1; PID:g17129845; GSPDB:G		
A:Experimental source: strain PCC 7120		
C:Genetics:		
A:Gene: asr0500		
Query Match		9.0%; Score 44.5; DB 2; Length 58;
Best Local Similarity		52.0%; Pred. No. 3.1e+02;
Matches		13; Conservative 3; Mismatches 8; Indels 1; Gaps 1;
QY	45 SLLEQ-SHSPSLYLQCLSQKURQE 68	
DB	13 SLLEQLSVTEQQEILQYLSQLHSQ 37	
Search completed: June 20, 2005, 14:03:57		
Job time : 40 secs		

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OM protein - protein search, using sw model

Run on: June 20, 2005, 13:45:42 ; Search time 172 Seconds
(without alignments)
285.812 Million cell updates/sec

Title: US-10-713-208-6_COPY_253_348

Perfect score: 497

Sequence: 1 LEDSSLLEVDGPAMKNVEPK.....ITSEKDMHFSSGLCILLDVL 96

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 234051

Minimum DB seq length: 0

Maximum DB seq length: 96

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	58	11.7	62	2	Q8VAX8	Q8vax8 white spot
2	57.5	11.6	91	2	Q8W459	Q8w459 arabidopsis
3	55.5	11.2	93	2	Q8ECX4	Q8ecx4 shewanella
4	55	11.1	78	2	Q7U750	Q7u750 synchococc
5	54	10.9	92	1	Y614_PASMU	Q9cn31 pasteurella
6	53	10.7	65	2	Q9ZG19	Q9zg19 chlamydia t
7	51	10.3	64	2	Q7R2F1	Q7r2f1 giardia lam
8	50.5	10.2	64	2	Q42305	Q42305 arabidopsis
9	50	10.1	90	2	Q7YR94	Q7yr94 bos taurus
10	50	10.1	92	2	Q8TQY7	Q8tg77 methanosarc
11	49.5	10.0	67	2	Q72DB9	Q72db9 desulfovibr
12	49.5	10.0	69	2	Q6IGM3	Q6igm3 sarcophaga
13	49.5	10.0	71	2	Q7TGT2	Q7t6t2 canine coro
14	49.5	10.0	94	2	Q9BF04	Q9bf04 tapirus ind
15	49.5	10.0	96	2	Q84NC6	Q84nc6 oryza sativ
16	49	9.9	63	2	Q6PZM3	Q6pzm3 human immun
17	49	9.9	63	2	Q6P2M4	Q6p2m4 human immun
18	49	9.9	74	2	Q8ZSF6	Q8zsf6 anabaena sp
19	49	9.9	92	2	Q8DUM3	Q8dum3 streptococc
20	48.5	9.8	68	2	Q8YSZ0	Q8ysz0 anabaena sp
21	48.5	9.8	74	2	Q95LE1	Q95le1 canis famli
22	48.5	9.8	75	2	Q9UBA7	Q9uba7 homo sapien
23	48.5	9.8	87	2	Q98672	Q98672 simian cyto
24	48.5	9.8	94	2	Q9BF05	Q9bf05 ceratotheri
25	48.5	9.8	95	2	Q6R4R2	Q6r4r2 brassica ol
26	48.5	9.8	95	2	Q6R4R3	Q6r4r3 brassica ol
27	48.5	9.8	95	2	Q6R4S0	Q6r4s0 brassica ol
28	48.5	9.8	95	2	Q6R4S2	Q6r4s2 brassica ol
29	48.5	9.8	95	2	Q6R4S4	Q6r4s4 brassica ra
30	48.5	9.8	95	2	Q6R4S5	Q6r4s5 brassica ra
31	48.5	9.8	96	2	Q89YD2	Q89yd2 bradyrhizob

32	48	9.7	51	2	Q9PDL5	Q9pdl5 xylella faa
33	48	9.7	54	2	Q7MQ15	Q7mq15 vibrio vuln
34	48	9.7	77	2	Q726J2	Q726j2 desulfovibr
35	48	9.7	87	2	Q6Z187	Q6z187 oryza sativ
36	47.5	9.6	59	2	Q9Y8C3	Q9y8c3 coprinus ci
37	47.5	9.6	60	1	HXB1_BRARE	O42366 brachydanio
38	47.5	9.6	65	1	IACA_PIG	P00999 sus scrofa
39	47.5	9.6	70	2	Q69TY7	Q69ty7 oryza sativ
40	47.5	9.6	83	2	Q8KK21	Q8kk21 proteus vul
41	47.5	9.6	85	2	Q9C676	Q9c676 arabidopsis
42	47.5	9.6	95	2	Q6XQA3	Q6xqa3 enterobacte
43	47	9.5	58	2	Q9P148	Q9p148 homo sapien
44	47	9.5	62	2	Q73D66	Q73d66 bacillus ce
45	47	9.5	64	2	Q7VAA8	Q7vaa8 prochloroco

ALIGNMENTS

RESULT 1

ID	Q8VAX8	PRELIMINARY;	PRT;	62 AA.
AC	Q8VAX8;			
DT	01-MAR-2002 (Tremblrel. 20, Created)			
DT	01-MAR-2002 (Tremblrel. 20, Last sequence update)			
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)			
DE	Wav241 (WSSV297).			
OS	White spot syndrome virus (WSSV).			
OC	Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.			
OX	NCBI_TaxID=92652;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21548311; PubMed=11689662;			
RX	DOI=10.1128/JVI.75.23.11811-11820.2001;			
RA	Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;			
RT	"Complete genome sequence of the shrimp white spot bacilliform			
RT	virus.";			
RL	J. Virol. 75:11811-11820(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20517548; PubMed=11062040; DOI=10.1006/viro.2000.0597;			
RA	Tsai M.F., Yu H.T., Tzeng H.F., Leu J.H., Chou C.M., Huang C.J.,			
RA	Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;			
RT	"Identification and characterization of a shrimp white spot syndrome			
RT	virus (WSSV) gene that encodes a novel chimeric polypeptide of			
RL	cellular-type thymidine kinase and thymidylate kinase.";			
RN	Virolgy 277:100-110(2000).			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21844071; PubMed=11853398; DOI=10.1006/viro.2001.1273;			
RA	Chen L.L., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,			
RA	Lo C.F., Kou G.H.;			
RT	"Identification of a nucleocapsid protein (VP35) gene of shrimp white			
RT	spot syndrome virus and characterization of the motif important for			
RL	targeting VP35 to the nuclei of transfected insect cells.";			
RN	Virolgy 293:44-53(2002).			
RP	SEQUENCE FROM N.A.			
RA	Lo C.-F., Kou G.-H.;			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBDJ databases.			
DR	EMBL; AF332093; AAL3245.1; -.			
DR	EMBL; AF440570; AAL89165.1; -.			
SQ	SEQUENCE 62 AA; 6698 MW; 9BBCCD06C5367855 CRC64;			

Query Match 11.7%; Score 58; DB 2; Length 62;

Best Local Similarity 31.8%; Pred. No. 48; Mismatches 5; Indels 22; Gaps 4;

Matches 21; Conservative 5; Mismatches 18; Indels 22; Gaps 4;

QY 21 AQKRGCLTVHREADFFWLSLCTADMSLLEQSHSSPSLYQLCS-----QKLRQERGTI-PG 74

Db 8 ADKRGITIKHMS-----WHLVADIS-----RECCSLFTTTAKTQSSGTTSPG 51

QY 75 SGITES 80


```
DR EMBL; AB006098; AAK02698.1; --
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 92 AA; 10340 MW; 304338CE07ECA377 CRC64;

Query Match
Best Local Similarity 10.9%; Score 54; DB 1; Length 92;
Matches 26; Conservative 16; Mismatches 33; Indels 24; Gaps 4;

QY 2 EDSLLVDPAMKVNVEFAKRGKLCIVHREADFFWSLCTAD-MSLLEQSHSP-----SLY 57
DB 7 QEKELLMKMDALRMKLYAQSKPKQVTPH-----FTPADSLSMIASSLNQPVVRSLSA 58
QY 58 LQCLSKLQRCQRTIFGSGITESKDMHFSGLGCLLDVL 96
DB 59 VSLLSKKL-----LSSKFLTYSALGMIALYLL 85

RESULT 6
Q9ZG19 PRELIMINARY; PRT; 65 AA.
AC Q9ZG19;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Dihydrofolate reductase/thymidylate synthase (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L2 434B;
RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF087357; AAD04129.1; --
DR MEROPS; M03.007; --
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001567; Pept_M3A_M3B.
DR Pfam; PF01432; Peptidase_M3; 1.
FT NON_TER 1
FT NON_TER 65
SQ SEQUENCE 65 AA; 7640 MW; C8F2D8FF255E63B8 CRC64;

Query Match
Best Local Similarity 10.7%; Score 53; DB 2; Length 65;
Matches 11; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 36 FWSLCTADMSLLEQSHSPSLYLQCLSKLRQ 67
DB 3 FWGSLRKSHPHSLALASLYMQSTDRELRK 34

RESULT 7
Q7R2F1 PRELIMINARY; PRT; 64 AA.
AC Q7R2F1;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP 623 54983 54789.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE OF 61-65 FROM N.A.
RC STRAIN=WB C6;
RX MEDLINE=20370943; PubMed=10908635;
RA Wu G., McArthur A.G., Fieer A., Saii A., Sogin M.L., Miller M.;
RT "Core histones of the amtochondriate protist, Giardia lamblia.";
RL Mol. Biol. Evol. 17:1156-1163 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;

RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC !- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB01000021; EAA41517.1; --
SQ SEQUENCE 64 AA; 7813 MW; 1F2077C5421D1FCE CRC64;

Query Match
Best Local Similarity 10.3%; Score 51; DB 2; Length 64;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 30 HREADFFWSLCTADMSLLEQ 49
DB 10 HAQNOFFWSFCLQKVLAE 29

RESULT 8
Q42305 PRELIMINARY; PRT; 64 AA.
AC Q42305;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Glycoprotein EPI - carrot (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurooids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cell suspension culture of ecotype columbia;
RA CNRS;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cell suspension culture of ecotype columbia;
RA Bardet C., Dabos P., Tremoussaygue D., Lescure B.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; 235737; CAA84803.1; --
FT NON_TER 1
FT NON_TER 64
SQ SEQUENCE 64 AA; 7730 MW; 6129171A1B5F27EE CRC64;

Query Match
Best Local Similarity 10.2%; Score 50.5; DB 2; Length 64;
Matches 12; Conservative 9; Mismatches 13; Indels 1; Gaps 1;

QY 38 SLCTADMSLLEQSHSPSLYLQCLSKLRQERTI 72
DB 22 SFCTSPFQLLFY-NTTPSVYILARVGLRDESTM 55

RESULT 9
Q7YR94 PRELIMINARY; PRT; 90 AA.
AC Q7YR94;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Sutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14667821; DOI=10.1016/S0888-7543 (03) 00238-6;
RA Winter A., Alzinger A., Fries R.;
```

[illegible]

```

Best Local Similarity 24.6%; Pred. No. 7.9e+02;
Matches 17; Conservative 12; Mismatches 19; Indels 21; Gaps 4

RESULT 13
Q7T6T2 PRELIMINARY; PRT; 71 AA.
ID Q7T6T2 AC
AT Q7T6T2 DT
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Non-structural protein 3a.
GN Name=nsP_3a;
OS Canine coronavirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; Group 1 species.
OX NCBI_TaxID=11153;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BGF10;
RX PubMed=15177889; DOI=10.1016/j.virusres.2004.02.038;
RA Sanchez-Morgado J.M., Poynter S., Morris T.H.;
RT "Molecular characterization of a virulent canine coronavirus BGF strain.";
RT Virus Res. 104:27-31(2004).
RL EMBL; AY342160; RAQ17221.1; -
DR InterPro; IPR006784; Corona_3.
DR Pfam; PF04694; Corona_3; 1.
SQ SEQUENCE 71 AA; 7706 MW; F89CAA3CC7D134D CRC64;

Query Match 10.0%; Score 49.5; DB 2; Length 71;
Best Local Similarity 26.6%; Pred. No. 5.6e+02;
Matches 17; Conservative 18; Mismatches 24; Indels 5; Gaps 2;

QY 34 DFFWLSLTADMSLLRQ---SHSSPSLYLQCISLQRGRTIPSGIGTESKDMHFSSLCG 90
DB 2 DIVKSIDSVDALDFEFCAGFAVTLKVFEKTGLLVCI GF--GDTILEAKDKAYAKLGC 59

QY 91 ILLD 94
DB 60 SIIE 63

RESULT 14
Q9BF04 PRELIMINARY; PRT; 94 AA.
ID Q9BF04 AC
AT Q9BF04 DT
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Prepronociceptin (Fragment).
GN Name=PNOc;
OS Tapirus indicus (Asiatic tapir) (Malayan tapir).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
OX NCBI_TaxID=9802;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21082082; PubMed=11214319; DOI=10.1038/35054550;
RX Murphy W.J., Ezirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011857; AAG38306.1; --
DR GO; GO:007218; P:neuropeptide signaling pathway; IEA.
DR GO; GO:0007268; P:synaptic transmission; IEA.
DR InterPro; IPR002367; Nociceptin.
DR InterPro; IPR006023; Opioid neuroep.
DR pfam; PF01160; Opiods neuroep; 2.
DR PRINTS; PR01031; ORPHNPCRSR.
FT NON_TER 1 1
FT TER 94 94
SQ SEQUENCE 94 AA; 10441 MW; 8FFIA35616592845 CRC64;

Query Match 10.0%; Score 49.5; DB 2; Length 94;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 13:44:57 ; Search time 158 Seconds
(without alignments)
234.994 Million cell updates/sec

Title: US-10-713-208-6_COPY_253_348
Perfect score: 497
Sequence: 1 LEDSSLEVDGPAKKNVEFK.....ITESKDMHFSSLCILLDVL 96

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1155283

Minimum DB seq length: 0
Maximum DB seq length: 96

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	353	71.0	76	4	AAM15359 Peptide #
2	353	71.0	76	4	Abb34356 Peptide #
3	353	71.0	76	4	Aam27837 Peptide #
4	353	71.0	76	4	Abb29199 Peptide #
5	353	71.0	76	4	Abb19775 Protein #
6	353	71.0	76	4	Aam67546 Human bon
7	353	71.0	76	4	Aam55153 Human bra
8	353	71.0	76	4	Abg49189 Human liv
9	353	71.0	76	4	Aam03118 Peptide #
10	353	71.0	76	5	Abg37140 Human pep
11	60	12.1	92	3	Aab33250 Eucalyptu
12	58	11.7	71	3	Aag60552 Arabidops
13	58	11.7	72	3	Aag56185 Arabidops
14	57.5	11.6	64	4	Aam90887 Human imm
15	57.5	11.6	78	3	Aag61267 Arabidops
16	57	11.5	73	8	Ades91199 c-Jun hom
17	57	11.5	83	8	Ades91198 c-Jun hom
18	57	11.5	89	2	Aaw82628 Ehrlichia
19	57	11.5	89	3	Aay78548 Ehrlichia
20	57	11.5	89	5	Aag93398 Ehrlichia
21	57	11.5	89	5	Aau73195 Human gra
22	56	11.3	86	5	Aau97011 Human GTP
23	55.5	11.2	68	6	Abj19123 Pathogen
24	55	11.1	75	5	Abp07109 Human ORF
25	55	11.1	77	6	Adb06692 Alloiococ

ALIGNMENTS

RESULT 1
AAM15359
ID AAM15359 standard; protein; 76 AA.

XX AAM15359;
XX
XX
DT 12-OCT-2001 (first entry)

DE Peptide #1793 encoded by probe for measuring cervical gene expression.

XX KW Probe; human; microarray; gene expression; cervical epithelial cell;
XX KM cervical cancer.

XX OS Homo sapiens.

XX PN WO200157278-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000670.

XX PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX PA Penn SG, Hanzel DK, Chen W, Rank DR;

XX PI WPI; 2001-488901/53.

XX DR Human genome-derived single exon nucleic acid probes useful for analyzing

XX PT gene expression in human cervical epithelial cells.

XX PS Claim 27; SEQ ID NO 20185; 487pp; English.

XX CC The present invention relates to human single exon nucleic acid probes

CC (SEN: see AAI10088-AAI28459). The present sequence is a peptide encoded

CC by one such probe. The SENPs are derived from human Hela cells. The SENPs

CC can be used to produce a single exon microarray, which can be used for

CC measuring human gene expression in a sample derived from human cervical

Aau59349 Propionib
Abm5868 Propionib
Abp28511 Streptoco
Aau51869 Propionib
Abm48388 Propionib
Abg03427 Novel hum
Adp30341 Human sec
Abg03792 Novel hum
Abg14805 Novel hum
Abg03922 Novel hum
Abj05481 Human bre
Adk34295 Novel hum
Add44488 Polypepti
Abol13991 Novel hum
Adm60688 Human sec
Aay27586 Human sec
Adg78397 Human sec
Aaw58844 Human AX9
Aau55575 Propionib
Abm52094 Propionib

CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 76 AA;

Query Match 71.0%; Score 353; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.7e-36;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEDSSILLEVDGPMKKNVEFKAKRGKGLCTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 60
DB 9 LEDSSILLEVDGPMKKNVEFKAKRGKGLCTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 68
QY 61 LSQKLQRE 68
DB 69 LSQKLQRE 76

RESULT 2
ABB34356
ID ABB34356 standard; peptide; 76 AA.
XX
AC ABB34356;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #1862 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000669.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
XX
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
PS Claim 27; SEQ ID NO 26991; 639pp + Sequence Listing; English.
XX
XX

CC The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 76 AA;

Query Match 71.0%; Score 353; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.7e-36;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEDSSILLEVDGPMKKNVEFKAKRGKGLCTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 60

DB 9 LEDSSILLEVDGPMKKNVEFKAKRGKGLCTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 68
QY 61 LSQKLQRE 68
DB 69 LSQKLQRE 76

RESULT 3
AAM27837
ID AAM27837 standard; protein; 76 AA.
XX
AC AAM27837;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #1874 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
XX
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
PS Claim 27; SEQ ID NO 28106; 654pp; English.
XX
XX

Query Match 71.0%; Score 353; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.7e-36;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEDSSILLEVDGPMKKNVEFKAKRGKGLCTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 60
DB 9 LEDSSILLEVDGPMKKNVEFKAKRGKGLCTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 68
QY 61 LSQKLQRE 68
DB 69 LSQKLQRE 76

RESULT 4
ABB29199
ID ABB29199 standard; peptide; 76 AA.

```
XX ABB29199;
AC
XX 01-FEB-2002 (first entry)
XX
XX Peptide #1850 encoded by breast cell single exon nucleic acid probe.
XX
XX Human; microarray; single exon probe; gene expression; breast; disease;
XX cancer.
XX
XX Homo sapiens.
XX
XX WO200157271-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000662.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-496933/54.
XX
XX New spatially-addressable set of single exon nucleic acid probes, useful
XX for measuring gene expression in sample derived from human breast,
XX comprises number of single exon nucleic acid probes.
XX
XX Claim 27; SEQ ID NO 12167; 327pp + Sequence Listing; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human breast and BT 474 cells. The method involves contacting the
XX probes with a collection of detectably labelled nucleic acids derived
XX from mRNA of human breast, and then measuring the label bound to each
XX probe of the microarray. The probes are useful for verifying the
XX expression of regions of genomic DNA predicted to encode proteins. They
XX are useful for gene discovery, and for determining predisposition and/or
XX prognosing breast disease. Gene expression analysis is useful for
XX assessing the toxicity of chemical agents on cells. The microarray of
XX this invention presents a far greater diversity of probes for measuring
XX gene expression, with far less bias than expressed sequence tag
XX microarrays. The method is suitable for rapid production of functional
XX information from genomic sequence. The present sequence is a peptide
XX encoded by a single exon nucleic acid probe of the invention. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 71.0%; Score 353; DB 4; Length 76;
XX Best Local Similarity 100.0%; Pred. No. 6.7e-36;
XX Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 LEDSSLEVDGPAKKNVFEKAKRGCTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 60
XX
XX 9 LEDSSLEVDGPAKKNVFEKAKRGCTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 68
XX
XX 61 LSQKLQRE 68
XX
XX 69 LSQKLQRE 76
XX
XX RESULT 5
XX
XX AAM67546
XX
XX AAM67546 standard; protein; 76 AA.
XX
XX AAM67546;
```

```
ABB19775
XX
XX ID ABB19775 standard; protein; 76 AA.
XX
XX AC ABB19775;
XX
XX 23-JAN-2002 (first entry)
XX
XX Protein #1774 encoded by probe for measuring heart cell gene expression.
XX
XX Human; gene expression; heart; microarray; vascular system;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease.
XX
XX Homo sapiens.
XX
XX WO200157274-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts.
XX
XX Claim 15; SEQ ID NO 21545; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart (see
XX ABA21535-ABA41305). The present sequence is a protein encoded by one such
XX probe. The probes may be used for predicting, measuring and displaying
XX gene expression in samples derived from the human heart via microarrays.
XX By measuring gene expression, the probes are useful for predicting,
XX diagnosing, grading, staging, monitoring and prognosing diseases of the
XX human heart and vascular system e.g. cardiovascular disease,
XX hypertension, cardiac arrhythmias and congenital heart disease. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 71.0%; Score 353; DB 4; Length 76;
XX Best Local Similarity 100.0%; Pred. No. 6.7e-36;
XX Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 LEDSSLEVDGPAKKNVFEKAKRGCTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 60
XX
XX 9 LEDSSLEVDGPAKKNVFEKAKRGCTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 68
XX
XX 61 LSQKLQRE 68
XX
XX 69 LSQKLQRE 76
XX
XX RESULT 6
XX
XX AAM67546
XX
XX AAM67546 standard; protein; 76 AA.
XX
XX AAM67546;
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XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 27852.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000668.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488900/53.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human bone marrow.
XX PS Example 4; SEQ ID NO 27852; 658pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC bone marrow. They can be used to measure gene expression in bone marrow
XX CC samples, which may enable the improved diagnosis and treatment of cancers
XX CC such as lymphoma, leukaemia and myeloma. The present sequence is a
XX CC protein encoded by one of the probes of the invention
XX SQ Sequence 76 AA;
    Query Match 71.0%; Score 353; DB 4; Length 76;
    Best Local Similarity 100.0%; Pred. No. 6.7e-36;
    Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEDSSILLEVDGPAMKNVFKAKRGICTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 60
Db 9 LEDSSILLEVDGPAMKNVFKAKRGICTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 68
QY 61 LSQKLQKE 68
Db 69 LSQKLQKE 76
RESULT 7
AAM55153
ID AAM55153 standard; protein; 76 AA.
XX AC AAM55153;
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe encoded protein SEQ ID NO: 27258.
XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;
XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX OS Homo sapiens.
XX PN WO200157275-A2.

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XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000667.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-483446/52.
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX PT brains.
XX PS Example 4; SEQ ID NO 27258; 650pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC brain. They can be used to measure gene expression in brain cell samples,
XX CC which may enable the diagnosis and improved treatment of nervous system
XX CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX CC epilepsy and cancers. The present sequence is a protein encoded by one of
XX CC the probes of the invention
XX SQ Sequence 76 AA;
    Query Match 71.0%; Score 353; DB 4; Length 76;
    Best Local Similarity 100.0%; Pred. No. 6.7e-36;
    Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEDSSILLEVDGPAMKNVFKAKRGICTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 60
Db 9 LEDSSILLEVDGPAMKNVFKAKRGICTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 68
QY 61 LSQKLQKE 68
Db 69 LSQKLQKE 76
RESULT 8
ABG49189
ID ABG49189 standard; peptide; 76 AA.
XX AC ABG49189;
XX DT 25-FEB-2003 (first entry)
XX DE Human liver peptide, SEQ ID No 27837.
XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX KW hypercholesterolaemia; coronary heart disease.
XX OS Homo sapiens.
XX PN WO200157273-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000664.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 21-SEP-2000; 2000US-00632366.
XX PR 03-AUG-2000; 2000US-0234687P.

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PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-48898/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
PT
XX Claim 27; SEQ ID NO 27837; 658pp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SNP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG59930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence
CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 76 AA;
XX
Query Match 71.0%; Score 353; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.7e-36;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEDSSILLEVDGPMKKNVEFKAKRGKGLCTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 60
DB 9 LEDSSILLEVDGPMKKNVEFKAKRGKGLCTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 68
QY 61 LSQKLRLQE 68
DB 69 LSQKLRLQE 76
RESULT 9
AAM03118
ID AAM03118 standard; protein; 76 AA.
XX
XX AAM03118;
AC
XX 09-OCT-2001 (first entry)
DT
XX Peptide #1800 encoded by probe for measuring breast gene expression.
DE
XX Probe; human; breast disease; breast cancer; development disorder;
XX inflammatory disease; proliferative breast disease; non-carcinoma tumour.
KW
XX Homo sapiens.
OS
XX WO200157270-A2.
PN
XX 09-AUG-2001.
PD
XX 29-JAN-2001; 2001WO-US000661.
PF
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
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PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-476286/51.
XX
XX Novel single exon nucleic acid probe used to measuring gene expression in
PT a human breast.
PT
XX Claim 27; SEQ ID NO 11858; 322pp; English.
XX
XX The present invention relates to novel single exon nucleic acid probes
CC (see AAI00010-AA110067). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for measuring human gene expression in
CC a human breast sample, where the probe hybridises at high stringency to a
CC nucleic acid expressed in the human breast. The probes are useful for
CC predicting, diagnosing, grading, staging, monitoring and prognosing
CC diseases of the human breast, particularly those diseases with polygenic
CC aetiology. The diseases include: breast cancer; disorders of development,
CC inflammatory diseases of the breast; fibrocystic changes; proliferative
CC breast disease and non-carcinoma tumours. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 76 AA;
XX
Query Match 71.0%; Score 353; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.7e-36;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEDSSILLEVDGPMKKNVEFKAKRGKGLCTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 60
DB 9 LEDSSILLEVDGPMKKNVEFKAKRGKGLCTVHREADFFWSLCTADMSLLEQSHSPSLYLQC 68
QY 61 LSQKLRLQE 68
DB 69 LSQKLRLQE 76
RESULT 10
ABG37140
ID ABG37140 standard; peptide; 76 AA.
XX
XX ABG37140;
AC
XX 19-AUG-2002 (first entry)
DT
XX Human peptide encoded by genome-derived single exon probe SEQ ID 26805.
DE
XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.
XX
XX Homo sapiens.
OS
XX WO200186003-A2.
PN
XX 15-NOV-2001.
PD
XX 30-JAN-2001; 2001WO-US000665.
PF
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
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PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2002-114183/15.
XX Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples.
XX
XX Claim 27; SEQ ID NO 26805; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC; the novel set of probes which hybridise at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of the
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Kargener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a peptide/protein encoded by a single exon probe of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 76 AA;
Query Match 71.0%; Score 353; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.7e-36;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEDSSLLLEVDGPAMKNVEFKAKRGICCTVHREADFWSLCTADMSLLEQSHSPSLYLQ 60
DB 1 LEDSSLLLEVDGPAMKNVEFKAKRGICCTVHREADFWSLCTADMSLLEQSHSPSLYLQ 68
QY 61 LSQKLQ 68
DB 69 LSQKLQ 76
RESULT 11
AAB33250
ID AAB33250 standard; protein; 92 AA.
XX
XX AAB33250;
AC

XX 25-JAN-2001 (first entry)
XX Eucalyptus grandis transcription factor protein sequence #407.
XX
XX Plant; transcription factor; gene expression; eucalyptus; pine; acacia;
KW poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;
KW basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;
KW homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;
KW type 2 Cys2His2; CCAAT box element; MYB.
XX
OS Eucalyptus grandis.
XX
XX WO2000053724-A2.
XX
XX 14-SEP-2000.
PD
XX 09-MAR-2000; 2000WO-US006112.
XX
XX 11-MAR-1999; 99US-00266513.
PR 18-AUG-1999; 99US-0149485P.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
PI Wood M, McGrath A, Shenk MA, Glenn M;
XX WPI; 2000-579369/54.
DR
XX New isolated polynucleotide encoding a plant transcription factor for
PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,
PT having modified gene expression or modified activity of a polypeptide.
XX
XX Claim 8; Page 694; 747pp; English.
XX
XX The present invention relates to novel plant transcription factors from
CC Eucalyptus grandis or Pinus radiata. The present sequence is one such
CC transcription factor. The transcription factor may be used to produce a
CC plant having modified gene expression such as a woody plant e.g. a
CC eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or
CC to modify the activity of a polypeptide in a plant. The transcription
CC factors of the present invention are members from the following families
CC of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic
CC helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain
CC zipper, LIM domain, AP2 and EREBs, zinc finger domains of type 2
CC Cys2His2, CCAAT box elements and MYB
XX
SQ Sequence 92 AA;
Query Match 12.1%; Score 60; DB 3; Length 92;
Best Local Similarity 28.4%; Pred. No. 30;
Matches 19; Conservative 17; Mismatches 27; Indels 4; Gaps 2;
QY 2 EDSSLLLEVDGPAMKNVEFKAKRGICCTVHREADFWSLCTADMSLLEQSHSPSLYLQCL 61
DB 4 EKIKIKIDNLTARQVTFKRRRLI---KKABELSVLCLADVSLVFS-ATGKLYDFSS 59
QY 62 SQKLQ 68
DB 60 SQMKGE 66
RESULT 12
AAG60552
ID AAG60552 standard; protein; 71 AA.
XX
XX AAG60552;
AC
XX 18-OCT-2000 (first entry)
DT
XX Arabidopsis thaliana protein fragment SEQ ID NO: 78442.
DE
XX Protein identification; signal transduction pathway; metabolic pathway;
KW

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

XX PR 05-MAR-1999; 99US-0123180P.

XX PR 09-MAR-1999; 99US-0123548P.

XX PR 23-MAR-1999; 99US-0125788P.

XX PR 25-MAR-1999; 99US-0126264P.

XX PR 29-MAR-1999; 99US-0126785P.

XX PR 01-APR-1999; 99US-0127462P.

XX PR 06-APR-1999; 99US-0128234P.

XX PR 08-APR-1999; 99US-0128714P.

XX PR 16-APR-1999; 99US-0129845P.

XX PR 19-APR-1999; 99US-0130077P.

XX PR 21-APR-1999; 99US-0130449P.

XX PR 23-APR-1999; 99US-0130510P.

XX PR 23-APR-1999; 99US-0130891P.

XX PR 28-APR-1999; 99US-0131449P.

XX PR 30-APR-1999; 99US-0132048P.

XX PR 04-APR-1999; 99US-0132407P.

XX PR 04-MAY-1999; 99US-0132484P.

XX PR 05-MAY-1999; 99US-0132485P.

XX PR 06-MAY-1999; 99US-0132486P.

XX PR 06-MAY-1999; 99US-0132487P.

XX PR 07-MAY-1999; 99US-0132863P.

XX PR 11-MAY-1999; 99US-0134256P.

XX PR 14-MAY-1999; 99US-0134218P.

XX PR 14-MAY-1999; 99US-0134219P.

XX PR 14-MAY-1999; 99US-0134221P.

XX PR 14-MAY-1999; 99US-0134370P.

XX PR 18-MAY-1999; 99US-0134768P.

XX PR 19-MAY-1999; 99US-0134941P.

XX PR 20-MAY-1999; 99US-0135124P.

XX PR 21-MAY-1999; 99US-0135353P.

XX PR 24-MAY-1999; 99US-0135629P.

XX PR 25-MAY-1999; 99US-0136021P.

XX PR 27-MAY-1999; 99US-0136392P.

XX PR 28-MAY-1999; 99US-0136782P.

XX PR 01-JUN-1999; 99US-0137222P.

XX PR 03-JUN-1999; 99US-0137528P.

XX PR 04-JUN-1999; 99US-0137502P.

XX PR 07-JUN-1999; 99US-0137724P.

XX PR 08-JUN-1999; 99US-0138094P.

XX PR 10-JUN-1999; 99US-0138540P.

XX PR 10-JUN-1999; 99US-0138847P.

XX PR 14-JUN-1999; 99US-0139119P.

XX PR 16-JUN-1999; 99US-0139452P.

XX PR 16-JUN-1999; 99US-0139453P.

XX PR 17-JUN-1999; 99US-0139492P.

XX PR 18-JUN-1999; 99US-0139454P.

XX PR 18-JUN-1999; 99US-0139455P.

XX PR 18-JUN-1999; 99US-0139456P.

XX PR 18-JUN-1999; 99US-0139457P.

XX PR 18-JUN-1999; 99US-0139458P.

XX PR 18-JUN-1999; 99US-0139459P.

XX PR 18-JUN-1999; 99US-0139460P.

XX PR 18-JUN-1999; 99US-0139461P.

XX PR 18-JUN-1999; 99US-0139462P.

XX PR 18-JUN-1999; 99US-0139463P.

XX PR 18-JUN-1999; 99US-0139750P.

XX PR 18-JUN-1999; 99US-0139763P.

XX PR 21-JUN-1999; 99US-0139817P.

XX PR 22-JUN-1999; 99US-0139899P.

XX PR 23-JUN-1999; 99US-0140353P.

XX PR 23-JUN-1999; 99US-0140354P.

PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 26-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
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(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

N-PSDB; AAK63668.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
useful for preventing, diagnosing and/or treating cancers and metastasis.

Claim 11; SEQ ID NO 18480; 3071pp + Sequence Listing; English.

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PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
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PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.

PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 11.6%; Score 57.5; DB 3; Length 78;

Best Local Similarity 32.2%; Pred. No. 50;

Matches 19; Conservative 6; Mismatches 19; Indels 15; Gaps 2;

QY 50 SHSPSLYLQCLSL-----QKLRQERG-----TIPGSGITESKMHFSSLCGILL 93

DB 5 SNSSSLFLTCLSSHLYLTIHKIRDRGVKSTGRATLTGFAEVNDVTMFQGLVRLMLM 63

Search completed: June 20, 2005, 14:00:15

Job time : 160 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2005, 14:03:24 ; Search time 157 Seconds
(without alignments)
234.790 Million cell updates/sec

Title: US-10-713-208-6_COPY_253_348

Perfect score: 497

Sequence: 1 LEDSSLEVDGPRAMKNVEFK.....ITFSKDMHPSLGCILLDVL 96

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 171042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 748755

Minimum DB seq length: 0

Maximum DB seq length: 96

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	353	71.0	76	9	US-09-864-761-35073
2	63	12.7	50	15	US-10-424-599-178808
3	60.5	12.2	86	16	US-10-437-963-140300
4	60	12.1	85	15	US-10-424-599-207479
5	60	12.1	92	16	US-10-856-499-2205
6	58.5	11.8	67	16	US-10-437-963-138338
7	58.5	11.8	87	17	US-10-424-599-208754
8	58.5	11.8	87	17	US-10-732-923-15868
9	58.5	11.8	94	15	US-10-424-599-193827
10	57.5	11.6	86	16	US-10-437-963-191300
11	57	11.5	89	9	US-09-159-469-26

12	57	11.5	89	9	US-09-798-042-26
13	57	11.5	89	9	US-09-953-108-26
14	57	11.5	96	15	US-10-424-599-206718
15	56	11.3	72	17	US-10-732-923-16396
16	55.5	11.2	62	16	US-10-425-115-204456
17	55.5	11.2	68	17	US-10-470-0488-448
18	55	11.1	78	16	US-10-437-963-102975
19	55	11.1	86	17	US-10-732-923-16811
20	54.5	11.0	66	17	US-10-732-923-16612
21	54	10.9	69	16	US-10-425-115-292382
22	54	10.9	75	16	US-10-437-963-104068
23	53.5	10.8	54	15	US-10-424-599-189111
24	53.5	10.8	77	17	US-10-732-923-16413
25	53.5	10.8	94	15	US-10-424-599-187873
26	53	10.7	51	15	US-10-424-599-194305
27	53	10.7	52	15	US-10-424-599-199976
28	53	10.7	54	15	US-10-424-599-267605
29	53	10.7	71	16	US-10-425-115-335204
30	53	10.7	79	16	US-10-437-963-102725
31	53	10.7	84	15	US-10-424-599-288479
32	52	10.5	45	15	US-10-424-599-225162
33	52	10.5	56	15	US-10-424-599-154704
34	52	10.5	67	16	US-10-425-115-284569
35	52	10.5	67	16	US-10-425-115-289356
36	52	10.5	68	16	US-10-425-115-247598
37	52	10.5	79	16	US-10-437-963-109948
38	52	10.5	83	15	US-10-424-599-219827
39	52	10.5	85	16	US-10-437-963-173719
40	52	10.5	88	16	US-10-425-115-244136
41	52	10.5	91	15	US-10-425-114-57053
42	51.5	10.4	41	14	US-10-074-475-241
43	51.5	10.4	62	15	US-10-424-599-176492
44	51.5	10.4	81	16	US-10-425-115-218448
45	51.5	10.4	86	15	US-10-424-599-280476

ALIGNMENTS

RESULT 1

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; Sequence 35073, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30

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Sequence 26, Appl
Sequence 26, Appl
Sequence 206718,
Sequence 16396, A
Sequence 204456,
Sequence 448, App
Sequence 102975,
Sequence 16811, A
Sequence 292382, A
Sequence 104068,
Sequence 189111,
Sequence 16413, A
Sequence 187873,
Sequence 194305,
Sequence 199976,
Sequence 267605,
Sequence 335204,
Sequence 102725,
Sequence 268479,
Sequence 25162,
Sequence 154704,
Sequence 284569,
Sequence 289356,
Sequence 247598,
Sequence 109948,
Sequence 219827,
Sequence 173719,
Sequence 244136,
Sequence 57053, A
Sequence 241, App
Sequence 176492,
Sequence 218448,
Sequence 280476,


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b      :      :      :      :      :      :      :      :      :      :
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APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; TITLE OF INVENTION: AND TREATMENT OF EHRlichia INFECTION
; FILE REFERENCE: 210121.439C7
; CURRENT APPLICATION NUMBER: US/09/798,042
; CURRENT FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Ehrlichia sp.
US-09-798-042-26

Query Match 11.5%; Score 57; DB 9; Length 89;
Best Local Similarity 24.6%; Pred. No. 66;
Matches 15; Conservative 9; Mismatches 17; Indels 20; Gaps 2;
QY 33 ADFFWSLCTADMSLLRQSHSPSLYLQCLSQKLQERGTPGSGITESKDMHFSSLGCTIL 92
Db 28 SFFFLYSTTDF-LCTRSHSCPDAY-----VTDKRPQVYAGCVY 67
QY 93 L 93
Db 68 I 68

RESULT 13
US-09-953-108-26
; Sequence 26, Application US/09953108
; Publication No. US20020086984A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G
; APPLICANT: Lodes, Michael J.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; TITLE OF INVENTION: AND TREATMENT OF EHRlichia INFECTION
; FILE REFERENCE: 210121.439C8
; CURRENT APPLICATION NUMBER: US/09/953,108
; CURRENT FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Ehrlichia sp.
US-09-953-108-26

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Best Local Similarity 24.6%; Pred. No. 66;
Matches 15; Conservative 9; Mismatches 17; Indels 20; Gaps 2;
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QY 93 L 93
Db 68 I 68

RESULT 14
US-10-424-599-206718
; Sequence 206718, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 206718
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_28694C.1.pap
US-10-424-599-206718

Query Match 11.5%; Score 57; DB 15; Length 96;
Best Local Similarity 28.7%; Pred. No. 72;
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QY 10 DGPAMKNVEFKAQKRGCTVHREADFFWSLCTADMSLL-EQSHSPSLYLQCLSQKLQKE 68
Db 23 DGSITKQV-----MSKMAEMINSLCGGDEKLMERTH---LLMAWCSRMAIROK 68
QY 69 ROTIPGSGITESKDMHFSSLGCTILLDV 95
Db 69 DGRWVECGIT-----TGCPLTDV 86

RESULT 15
US-10-732-923-16396
; Sequence 16396, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 16396
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Glycine max
US-10-732-923-16396

Query Match 11.3%; Score 56; DB 17; Length 72;
Best Local Similarity 24.2%; Pred. No. 67;
Matches 16; Conservative 14; Mismatches 26; Indels 10; Gaps 2;
QY 5 SLLEVDGPAMKNVEFKAQKRGCTVHREADFFWSLCTADMSLLEQS-----HSSPSLY 57
Db 7 AIRRIDNSTSRQVTFKRRNGLLKKARELSI---LCDAEVGLMVFSSTKLYDYASTSRP 63
QY 58 LOCLSQ 63
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Job time : 161 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Run on: June 20, 2005, 13:54:53 ; Search time 43 Seconds
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166.658 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 320760

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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7	57	11.5	89	4	US-09-693-542-26
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9	51.5	10.4	75	4	US-09-621-976-7393
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11	50	10.1	47	4	US-09-139-600-47
12	50	10.1	47	4	US-09-989-903-52
13	50	10.1	88	4	US-09-583-110-4281
14	50	10.1	88	4	US-09-107-433-3932
15	50	10.1	96	4	US-09-107-532A-4733
16	49.5	10.0	63	4	US-09-543-681A-5822
17	49	9.9	80	4	US-09-248-796A-23290
18	49	9.9	82	3	US-08-905-223-481
19	48.5	9.8	96	2	US-08-737-560A-9
20	47.5	9.6	51	3	US-09-052-089A-5
21	47.5	9.6	72	4	US-09-270-767-60440
22	47.5	9.6	86	4	US-09-621-976-4271
23	47.5	9.6	61	4	US-09-270-767-44962
24	47	9.5	61	4	US-09-248-796A-23862
25	47	9.5	78	4	US-09-248-796A-24764
26	47	9.5	88	4	US-09-587-637B-41
27	47	9.5	88	4	US-09-248-796A-25988

Sequence 6902, Ap
Sequence 39923, A
Sequence 55140, A
Sequence 40507, A
Sequence 55723, A
Sequence 23700, A
Sequence 27825, A
Sequence 4811, Ap
Sequence 6964, Ap
Sequence 94, Appl
Sequence 2343, Ap
Sequence 23107, A
Sequence 19774, A
Sequence 1005, Ap
Sequence 5789, Ap
Patent No. 5514582
Patent No. 5514582

ALIGNMENTS

RESULT 1

US-09-640-211A-2205
; Sequence 2205, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2205
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-640-211A-2205

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Matches 19; Conservative 17; Mismatches 27; Indels 4; Gaps 2;

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DB 4 EKIKKIDNLTARQVTFKRRRLI---KKAELSVLCDADVSLIVFS-ATGKLYDFSS 59

QY 62 SQKLRQE 68
DB 60 SQQMKGE 66

RESULT 2

US-08-975-762-26
; Sequence 26, Application US/08975762
; Patent No. 6207169
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington

TREATMEN

/ COUNTRY: USA
/ ZIP: 98104
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/975,762
/ FILING DATE: 21-MAR-1997
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Maki, David J.
/ REGISTRATION NUMBER: 31,392
/ REFERENCE/DOCKET NUMBER: 210121.439
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-622-4900
/ TELEFAX: 206-682-6031
/ INFORMATION FOR SEQ ID NO: 26:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 89 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ ORIGINAL SOURCE:
/ ORGANISM: Ehrlichia
/ US-08-975-762-26

Query Match 11.5%; Score 57; DB 3; Length 89;
Best Local Similarity 24.6%; Pred. No. 6.7;
Matches 15; Conservative 9; Mismatches 17; Indels 20; Gaps 2;

QY 33 ADFWLSLCTADMSLLEQSHSPSLYLQCLSQKLRQERTIPGSGITESKDMHFSSLGCIL 92
Db 28 SSFFFLYSTTDF-LCTRSHSCPDAY-----VTDKQPQVYAAGCVY 67

QY 93 L 93
Db 68 I 68

RESULT 3

US-08-821-324-26
/ Sequence 26, Application US/08821324
/ Patent No. 6231869
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Lodes, Michael J.
/ APPLICANT: Houghton, Raymond
/ TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
/ NUMBER OF SEQUENCES: 38
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/821,324

FILING DATE: 21-MAR-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.439

TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 206-622-4900
/ TELEFAX: 206-682-6031
/ INFORMATION FOR SEQ ID NO: 26:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 89 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ ORIGINAL SOURCE:
/ ORGANISM: Ehrlichia
/ US-08-821-324-26

Query Match 11.5%; Score 57; DB 3; Length 89;
Best Local Similarity 24.6%; Pred. No. 6.7;
Matches 15; Conservative 9; Mismatches 17; Indels 20; Gaps 2;

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Db 28 SSFFFLYSTTDF-LCTRSHSCPDAY-----VTDKQPQVYAAGCVY 67

QY 93 L 93
Db 68 I 68

RESULT 4

US-09-295-028-26
/ Sequence 26, Application US/09295028
/ Patent No. 6277381
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Lodes, Michael J.
/ APPLICANT: Houghton, Raymond L.
/ APPLICANT: McNeill, Patricia D.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS

FILE REFERENCE: 210121.439C4

CURRENT APPLICATION NUMBER: US/09/295,028

CURRENT FILING DATE: 1999-04-20

NUMBER OF SEQ ID NOS: 85

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 26

LENGTH: 89

TYPE: PRT

ORGANISM: Ehrlichia sp.

US-09-295-028-26

Query Match 11.5%; Score 57; DB 3; Length 89;
Best Local Similarity 24.6%; Pred. No. 6.7;
Matches 15; Conservative 9; Mismatches 17; Indels 20; Gaps 2;

QY 33 ADFWLSLCTADMSLLEQSHSPSLYLQCLSQKLRQERTIPGSGITESKDMHFSSLGCIL 92
Db 28 SSFFFLYSTTDF-LCTRSHSCPDAY-----VTDKQPQVYAAGCVY 67

QY 93 L 93
Db 68 I 68

RESULT 5

US-09-106-582-26
/ Sequence 26, Application US/09106582
/ Patent No. 6306402
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Lodes, Michael J.
/ APPLICANT: Houghton, Raymond

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND

NUMBER OF SEQUENCES: 73

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

US-09-106-582-26

THERAPY

STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,582
FILING DATE: 29-JUN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.439C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 89 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Ehrlichia
US-09-106-582-26

Query Match 11.5%; Score 57; DB 3; Length 89;

Best Local Similarity 24.6%; Pred. No. 6.7;

Matches 15; Conservative 9; Mismatches 17; Indels 20; Gaps 2;

QY 33 ADFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQERTIPGSGITESKDMHFSSLCIL 92
DB 28 SSFFFLYSTDF-LCTRSHSCPDAY-----VTDKAPQVFAAGCVY 67

QY 93 L 93

DB 68 I 68

RESULT 6

US-09-159-469-26

Sequence 26, Application US/09159469

Patent No. 6607728

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Lodes, Michael J.

APPLICANT: Houghton, Raymond

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND

TITLE OF INVENTION: THERAPY OF EHRlichia INFECTION

NUMBER OF SEQUENCES: 73

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED AND BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/159,469

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/106,582
FILING DATE: 29-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.439C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 89 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Ehrlichia
US-09-159-469-26

Query Match 11.5%; Score 57; DB 4; Length 89;

Best Local Similarity 24.6%; Pred. No. 6.7;

Matches 15; Conservative 9; Mismatches 17; Indels 20; Gaps 2;

QY 33 ADFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQERTIPGSGITESKDMHFSSLCIL 92
DB 28 SSFFFLYSTDF-LCTRSHSCPDAY-----VTDKAPQVFAAGCVY 67

QY 93 L 93

DB 68 I 68

RESULT 7

US-09-693-542-26

Sequence 26, Application US/09693542

Patent No. 6673356

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Lodes, Michael J.

APPLICANT: Houghton, Raymond L.

APPLICANT: McNeill, Patricia D.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS

TITLE OF INVENTION: AND TREATMENT OF EHRlichia INFECTION

FILE REFERENCE: 210121.439C6

CURRENT APPLICATION NUMBER: US/09/693,542

CURRENT FILING DATE: 2000-10-20

NUMBER OF SEQ ID NOS: 89

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 26

LENGTH: 89

TYPE: PRT

ORGANISM: Ehrlichia sp.

US-09-693-542-26

Query Match

11.5%; Score 57; DB 4; Length 89;

Best Local Similarity 24.6%; Pred. No. 6.7;

Matches 15; Conservative 9; Mismatches 17; Indels 20; Gaps 2;

QY 33 ADFWSLCTADMSLLEQSHSPSLYLQCLSQKLRQERTIPGSGITESKDMHFSSLCIL 92
DB 28 SSFFFLYSTDF-LCTRSHSCPDAY-----VTDKAPQVFAAGCVY 67

QY 93 L 93

DB 68 I 68

RESULT 8

US-09-248-796A-25093

Sequence 25093, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

```
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 25093
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-25093

Query Match      11.2%; Score 55.5; DB 4; Length 64;
Best Local Similarity 40.5%; Pred. No. 6.7;
Matches 15; Conservative 5; Mismatches 12; Indels 5; Gaps 2;

QY      6 LLEVDGPAKMWVEKFAKRGGLCT---VHREADFFWS 38
Db      13 LLEFDKKIKNNKIKYKQ-TCTLQQLVHTENDSLWS 48

RESULT 9
US-09-621-976-7393
; Sequence 7393, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Maline Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSEI.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 7393
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 4
; OTHER INFORMATION: Xaa = Ala,Asp,Gly,Val
US-09-621-976-7393

Query Match      10.4%; Score 51.5; DB 4; Length 75;
Best Local Similarity 25.4%; Pred. No. 29;
Matches 15; Conservative 12; Mismatches 23; Indels 9; Gaps 1;

QY      12 PAKMWVEKFAKRGGLCTVHRE-----ADFFWSLCTADMSLLEQSHSPSYLQCL 61
Db      17 PLPOHIHFOSSARNLCAENRRKAQGAALPTGPFHSQASSAKAGREETHSPNPYDQGL 75

RESULT 10
US-09-187-789-52
; Sequence 52, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 52
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-989-903-52

Query Match      10.1%; Score 50; DB 4; Length 47;
Best Local Similarity 33.3%; Pred. No. 24;
Matches 12; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY      32 EADFFWSLCTADMSLLEQSHSPSYLQCLSQKLKQ 67
Db      10 EADFLGMATVLMCVSYRDPVNGTWIQLCSLRE 45

RESULT 11
US-09-139-600-47
; Sequence 47, Application US/09139600
; Patent No. 6432628
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434
; CURRENT APPLICATION NUMBER: US/09/139,600
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-47

Query Match      10.1%; Score 50; DB 4; Length 47;
Best Local Similarity 33.3%; Pred. No. 24;
Matches 12; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY      32 EADFFWSLCTADMSLLEQSHSPSYLQCLSQKLKQ 67
Db      10 EADFLGMATVLMCVSYRDPVNGTWIQLCSLRE 45

RESULT 12
US-09-989-903-52
; Sequence 52, Application US/09989903
; Patent No. 6797812
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434D1
; CURRENT APPLICATION NUMBER: US/09/989,903
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-989-903-52

Query Match      10.1%; Score 50; DB 4; Length 47;
Best Local Similarity 33.3%; Pred. No. 24;
Matches 12; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY      32 EADFFWSLCTADMSLLEQSHSPSYLQCLSQKLKQ 67
Db      10 EADFLGMATVLMCVSYRDPVNGTWIQLCSLRE 45
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RESULT 13
US-09-583-110-4281
; Sequence 4281, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4281
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4281

Query Match 10.1%; Score 50; DB 4; Length 88;
Best Local Similarity 29.3%; Pred. No. 58;
Matches 22; Conservative 9; Mismatches 22; Indels 22; Gaps 4;

QY 11 GPAMKNVEFKAQKR-----GLCTVHREADFFWS-----LCTADMSLLEQSHSSPS 55
DB 3 GDGMKEFQERKQFSLRPAIGACSVLLGTSLFFAGMGAPVQDTETSSALISSH---- 58

QY 56 LYL--OCLSKLRQE 68
DB 59 -YLDEQDLSEKLKSE 72

RESULT 14
US-09-107-433-3932
; Sequence 3932, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3932:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 88 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...88
; SEQUENCE DESCRIPTION: SEQ ID NO: 3932:
US-09-107-433-3932

Query Match 10.1%; Score 50; DB 4; Length 88;
Best Local Similarity 29.3%; Pred. No. 58;
Matches 22; Conservative 9; Mismatches 22; Indels 22; Gaps 4;

QY 11 GPAMKNVEFKAQKR-----GLCTVHREADFFWS-----LCTADMSLLEQSHSSPS 55
DB 3 GDGMKEFQERKQFSLRPAIGACSVLLGTSLFFAGMGAPVQDTETSSALISSH---- 58

QY 56 LYL--OCLSKLRQE 68
DB 59 -YLDEQDLSEKLKSE 72

RESULT 15
US-09-107-532A-4733
; Sequence 4733, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4733:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:

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; ORGANISM: Enterococcus faecium
;
; FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (B) LOCATION 1...96
;   SEQUENCE DESCRIPTION: SEQ ID NO: 4733:
US-09-107-532A-4733

Query Match      10.1%; Score 50; DB 4; Length 96;
Best Local Similarity 23.2%; Pred. NO. 65;
Matches 13; Conservative 15; Mismatches 24; Indels 4; Gaps 1;

QY      14 MKNVEFKAKRGICTVHRE----ADFFWSLCTADMSLLEQSHSPSLYLQCLSQKL 65
      ::::| | :| | : | | | : : : : | : | : | : |
Db      2 VRHMEIKKEKNRLALFNDEQQBIGEMTWS DAGFDIMIIDHTTFVDPAYRGQKLAEXL 57
      ::::| | :| | : | | | : : : : | : | : | : |

Search completed: June 20, 2005, 14:04:44
Job time : 44 secs
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